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US-09-579-664B-11; Sequence 11, Application US/09579664B
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Sequence 11, Appl
Sequence 11, Appl
                                                                                                    January 22, 2005, 06:30:32; Search time 16.3133 Seconds (without alignments) 1028.511 Million cell updates/sec
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1 YEFLETLGKGTYGKVKKARE......VNPTRRATLEDVASHWWVNW
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTTUS_COMB.pep:*
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Compugen Ltd.
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US-10-355-975A-11

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US-09-584-890-4

US-09-984-890-4

US-09-538-849-36

US-09-538-849-36

US-09-538-849-36

US-09-538-849-36

US-09-538-849-32

US-09-633-328B-2

US-09-633-328B-3

US-09-799-875-5

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             GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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Sequence 1841, A Sequence 34, Appl Sequence 2, Appli Sequence 2, Appli Sequence 154, Appl Sequence 28, Appl Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 6, Appli
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Patent No. 675923

GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Immunex Corporation
APPLICANT: Martin, Unia
APPLICANT: Martin, Unia
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
FILE REFERENCE: 2923-B
CURRENT APPLICATION NUMBER: US/10/355,975A
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 38
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US-09-248-796A-18441
US-09-248-796A-18441
US-10-103-626-2
US-10-003-690-2
US-09-930-181-2
US-09-538-092-154
US-09-538-092-154
US-09-248-27
US-07-857-2248-27
US-07-857-2248-27
US-09-238-49-2
US-09-238-49-2
US-09-238-49-2
US-09-248-796A-18435
US-09-248-796A-18435
US-09-248-796A-18435
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Best Local Similarity 100.0
Matches 253; Conservative
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117 IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 176
                                                                                                                                                                                     SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
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TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAK-1
TITLE OF INVENTION: KINASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,298 FILING DATE: 09-UUL-1996 CLASSIFICATION: 536 CLASSIFICATION: 536 NAME: CATUCHERS, Jennie M. REGISTRATION NUMBER: 34,464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.4%; Score 649.5; DB 3
51.6%; Pred. No. 3.2e-58;
cive 42; Mismatches 78
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S: 5370 Manhattan Circle, Suite 201
Boulder
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OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5863729
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TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 2: SEGUENCE CHARACTERISTICS:
LENGTH: 729 amino acids
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Best Local Similarity 51.64
Matches 131; Conservative
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COMPUTER READABLE FORM:
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APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: Marcin, Unja
APPLICANT: Marcin, Unja
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
FILE REFERENCE: 2923-B
CURRENT FILING DATE: 203-01-30
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                APPLICANT: Unmunex Corporation
APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: Wirca, G. Duke
APPLICANT: Wartin, Unja
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REPERENCE: 2923-A
CURRENT APPLICATION NUMBER: US/09/579,664B
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                           Score 1342; DB 4;
Pred. No. 7.7e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Best Local Similarity 100
Matches 253; Conservative
                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Mus musculus
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Patent No. 6514719
GENERAL INFORMATION:
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Sequence 4, Application US/10274194

Batent No. 6706511

CENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLO01306DIV

CURRENT APPLICATION NUMBER: US/10/274,194

CURRENT PILING DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                          IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHONGI 119
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                                                                                                                                                                                                                                                         120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTR 238
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                                                                                                                                                              Length 722;
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                                                                                                                                                              DB 4;
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48.2%; Score 647.5; DB 4;
Best Local Similarity 51.2%; Pred. No. 5.1e-58;
Matches 130; Conservative 44; Mismatches 77;
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                                                                                                                                                            48.2%; Score 647.5; DB 4
51.2%; Pred. No. 5.1e-58;
ative 44; Mismatches 77
                 NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
 2001-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 RGTLEQIMKDRWMN 305
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US-10-274-194-4
                                                                    LENGTH: 722
TYPE: PRT
CORGANISM: Rattus norvegicus
US-09-984-890-4
                                                                                                                                                           Query Match
Best Local Similarity 51.2*
Matches 130; Conservative
CURRENT FILING DATE:
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Patent No. 6492156

GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF LINVENTION: THEREOF

FILE REFERENCE: CL001306

CURRENT APPLICATION NUMBER: US/09/984,890
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                                  VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
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OTHER INFORMATION: GenBank Accession No. 6458561 g3089349
                                                                                                                                                                                                                                                             APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Molteni, Angela
APPLICANT: Magnaghi, Paola
APPLICANT: Bosotti, Roberta
APPLICANT: Bosotti, Roberta
APPLICANT: Bacchi, Antonella
APPLICANT: Hodgson, Dave
TITLE OF INVENTION: HUMAN NIMI KINASE
FILE REFERENCE: PC-0009 US
CURRENT APPLICATION NUMBER: US/09/523,849
CURRENT FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PERL Program
SOFTWARE: PERL Program
SENGTH: 729
                                                                                                                                                                                             5-09-523-849-33
Sequence 33, Application US/09523849
Patent No. 645851
GENERAL INFORMATION:
                                                                                                                       295 RGTLEQIMKDRWIN 308
                                                                                     RATLEDVASHWWVN 252
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 131; Conserval
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US-09-984-890-4
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GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THERE WOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERE OF
FILE REFERENCE: CLOOLISO
CURRENT APPLICATION NUMBER: US/09/984,890
CURRENT FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTMARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 IIAIHEVPENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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                                                                                                                                                                                                                                                       Length 713;
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                                                                                                                                              ; NAME/KEY: misc_feature
}, LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P27448
US-09-538-092-1022
                                                                                                                                                                                                                                                     Query Match
48.2%; Score 646.5; DB 4;
Best Local Similarity 51.6%; Pred. No. 6.3e-58;
Matches 131; Conservative 41; Mismatches 79;
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48.2%; Score 646.5; DB 4;
Best Local Similarity 50.8%; Pred. No. 6.4e-58;
Matches 129; Conservative 45; Mismatches 77;
                 CuraPatSegFormatter Version 0.9
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Patent No. 6492156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 RATLEDVASHWWVN 252
NUMBER OF SEQ ID NOS: 1387
                                                                           TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
               SOFTWARE: Cur
                                                         LENGTH: 713
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Patent No. 6753314

GENERAL INPORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REPERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT PILING DATE: 2006-03-29
PRIOR PRILING DATE: 1999-04-01
PRIOR PILING DATE: 2000-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank Accession No. 6458561 g1749794
US-09-523-849-36
                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Magnaghi, Paola
APPLICANT: Magnaghi, Paola
APPLICANT: Scacheri, Emanuela
APPLICANT: Scacheri, Emanuela
APPLICANT: Hodgson, Dave
IITLE OF INVENTION: HUMAN NIMI KINASE
FILE REFERENCE: PC-0009 US
CURRENT APPLICATION NUMBER: US/09/523,849
CURRENT FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PERL Program
SOFTWARE: PERL Program
SCAC DI NO 36
LENGTH: 745
                                                                                                                                                              Sequence 36, Application US/09523849
Patent No. 6458561
           239 RATLEDVASHWWVN 252
                                                   292 RGTLEQIMKDRWMN 305
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                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT: YAN, Chunhua et al.
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION:
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01306DIV
CURRENT APPLICATION NUMBER: US/10/274,194
CURRENT PILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTR 238
                 60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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Fatent No. 6777587
GENERAL IRPORANTION:
APPLICANT: BISARO, DAVID A.
TITLE OF INVENTION: METHOD OF ENHANCING PLANT RESISTANCE TO PATHOGENS
FILE REFERENCE: 22277-04041
CURRENT FILING DATE: 2000-08-07
FRIOR REPLICATION NUMBER: 60/147,613
PRIOR APPLICATION NUMBER: 60/147,613
FRIOR RELIGNED DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VOY: 3.2
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50.8%; Pred. No. 6.4e-58;
iive 45; Mismatches 77
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; Sequence 2, Application US/10274194
; Patent No. 6706511
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                                                                  239 RATLEDVASHWWVN 252
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US-10-274-194-2
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nes 129; Conserv
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US-09-633-328B-2
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LENGTH: 512
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60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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; Score 644; DB 4; Length 512;
; Pred. No. 7.1e-58;
47; Mismatches 75; Indels
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No. 6579691el Protein Kinase (NPK-110)
132
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STREET: 233 S. Wacker Drive, 6300 Sears Tower
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.9%; Score 642.5; DB 4; 50.8%; Pred. No. 1.7e-57;
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FILING DATE: 30-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11 7122.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/817,832B
FILING DATE: 28-APR-1997
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; Patent No. 6579691
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APPLICANT: MANDELKOW, Eckhard,
TITLE OF INVENTION: NO. 657969
NUMBER OF SEQUENCES: 32
    50.8%;
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RITIPEIROHRW 271
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CITY: Chicago
STATE: Illinois
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                           Best Local Sim
Matches 128;
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                                                                 60 IIAIHEVPENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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; OTHER INFORMATION: GenBank Accession No. 6458561 g2052189
US-09-523-849-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.9%; Score 642.5; DB 4
51.2%; Pred. No. 1.9e-57;
ilve 43; Mismatches 78
                                                                                                                                                                                                                                                          Sequence 32, Application US/09523849
Patent No. 6458561
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Banganghi, Paola
APPLICANT: Bosotti, Roberta
APPLICANT: Bosotti, Roberta
APPLICANT: Bosotti, Antonella
APPLICANT: Bosotti, Antonella
APPLICANT: Hodgson, Dave
ITTLE OF INVENTION: HUMAN NIMI KINASE
FILE REFERENCE: PC-0009 US
CURRENT APPLICATION NUMBER: US/09/523,849
CURRENT APPLICATION NUMBER: US/09/523,849
CURRENT PILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PERL Program
SSOFTWARE: PERL Program
SSOFTWARE: PERL Program
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US-09-633-328B-4
; Sequence 4, Application US/09633328B
; Patent No. 6777587
; GENERAL INFORMATION:
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RGSLEQIMKDRWMN 312
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ORGANISM: Rattus norvegicus
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Matches 130; Conservative
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                         APPLICANT: BISARO, DAVID A.

TITLE OF INVENTION: METHOD OF ENHANCING PLANT RESISTANCE TO PATHOGENS FILE REPERENCE: 22727-04041

CURRENT APPLICATION NUMBER: US/09/633,328B

CURRENT FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: 60/147,613

PRIOR FILING DATE: 1999-08-06

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN VET: 3.2

SEQ ID NO 4
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47.0%; Score 631; DB 4;
Best Local Similarity 49.6%; Pred. No. 1.6e-56;
Matches 125; Conservative 48; Mismatches 77,
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he: 17.3133 secs
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; ORGANISM: Nicotiana benthamiana
US-09-633-328B-4
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Aae19885 Rat SNF1/
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1422.048 Million cell updates/sec
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Adn95766 N
Aae07847 N
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Ade38421 H
Adj75331 N
Adl25353 H
Adq19734 H
Aab71959 H
Abb67451 I
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                   2002273 segs, 358729299 residues
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                                                                    protein search, using sw model
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ABU53319
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1 YBFLETLGKGTYGKVKKARE....
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Gapop 10.0 , Gapext 0.5
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Abp96068 Human pro	ABP96068	761 6	48.7	653	45
	ABB04431	724 5	7	6.099	44
_	ADG91727	688 7	49.2	660.5	43
Human	ADG91726		7	6.099	42
Aae33555 Human mic	AAE33555		7	6.099	41
Aae33554 Human mic	AAE33554		7	660.5	40
	ABB04432		7	6.099	39
Adj96622 Human cal	ADJ96622		m	661.5	38
Abp62966 Human pol	ABP62966		9	665.5	37
Human	ADL32125	752 8	9	665.5	36
Abg73794 Human MAR	ABG73794		و	665.5	35
Human	ABB04433	752 5	و	665.5	34
Aaell782 Human kin	AAE11782	752 4	9	665.5	33
Aam93956 Human pol	AAM93956	752 4	9	665.5	32
Human	ADF74129	•	9	665.5	31
Abb04434 Human neu	ABB04434	688 5	9	665.5	30
Mouse	ADI29235		9	665.5	29
Aab65629 Novel pro	AAB65629	520 4	و	665.5	28
Abg79179 Human ser	ABG79179	508 5	و	665.5	27
Aae00668 Human pro	AAE00668	530 4	7	814	56

ALIGNMENTS

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The present sequence is Murine Lymph node Stromal cell kinase 1 (MLSK-1). This protein is useful for treating a variety of disorders listed in the disclosure of the specification, including autoimmune disorders, allergic reactions, myeloid or lymphoid cell deficiencies, wound healing and tissue repair and replacement, burns, incisions and ulcers, periodontal disease, inflammatory diseases, tumours and bacterial, viral or fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses.
                                                                                                                                      Murine; Lymph node Stromal cell kinase; MLSK-1; autoimmune disorder; wound healing; periodontal disease; inflammatory disease; tumour; infection; allergy.
                                                                                                                                                                                                                                                                                                                                                                            Martin U, Anderson DM;
                                                                                                             Murine Lymph node Stromal cell kinase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 94-96; 106pp; English.
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                           631
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                         AAB50056 standard; protein;
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                                                       AAB50056;
RESULT 1
               AAB50050
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100.0%; Score 1342; DB 4; Length 631;

Sequence 631 AA;

Query Match

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                                                           1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
                                                                                 177 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLOTFCGSPLYASPEIVNGKPYVGPEVD
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/note= |"Serine/threonine protein kinase active-site"
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/note= "Serine/threonine kinase catalytic domain"
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                           Indels
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100.0%; Preα. ...
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12-MAR-2001; 2001US-0274613P.
28-MAR-2001; 2001CA-02340783.
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/note= "Se
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/note= |"Se
                         253; Conservative
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608. .6]
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Binding-site
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       Best Local
Matches 25
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The invention relates to an AMPK (AMP-activated protein kinase) related kinase, designated SNARK polypeptides and polynucleotides. SNARK (SNIF/AMP-activated protein kinase) is involved in stress response to glucose deprivation. The polynucleotides are useful for expressing SNARK protein in isolated form or as a protein conjugate. Activation of SNARK stimulates liver CPT-1 thus enhances lipid metabolism in liver cells and in other cell types such as heart and skeletal muscles, as well as in orbases GLUT-4 and glycogen in muscle. Activation of SNARK is predicted to have insulin-like effects that would enhance the disposal of glucose into muscle and reduce plasma glucose for the treatment of diabetes and come type of disorders of lipoprotein production leading to increased leaves of cholesterol or triglycerides. SNARK or its variants may be administered to a subject to treat or prevent a disease associated with decreased expression of SNARK, such as diabetes. SNARK antibodies are used to modulate SNARK activity either in vivo for therapeutic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        decrease glucose uptake and increase levels of blood glucose in a patier
suffering from hypoglycaemia. The present sequence is rat SNARK protein
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                                                                                                                                                                                                                                                                          AMPK (AMP-activated protein kinase)-related kinase, designated SNARK polypeptides and polynucleotides, useful for treating or preventing diabetes, or other disorders of lipoprotein production leading to increased levels of cholesterol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucose uptake and increase levels of blood
                                                                               Lefebvre DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 2; 94pp; English
(ONEO-) 1149336 ONTARIO INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253
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                                                                          Drucker DJ, Rosen CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TLEDVASHWWVNW
                                                                                                                                                          WPI; 2002-241747/29.
N-PSDB; AAD31710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 630 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
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from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a polypeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention describes novel polynucleotides and polypeptides isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 YEFLETIGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
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                                                   gene therapy; vaccine; disease treatment; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
              -fuman cell cycle-associated protein from DKFZphtes3_7j3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.3%; Score 1293; DB 4;
95.7%; Pred. No. 6.5e-133;
iive 6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                (GEHU-) GERMAN HUMAN GENOME PROJECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 21; Page 943; 1095pp; English.
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                                                                                                                                                                                                                                                    99US-0149499P.
                                                                                                                                                                                                             18-AUG-2000; 2000WO-IB001496
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Best Local Similarity 95.7
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            2001-327840/34.
                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABX71420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 628 AA;
                                                                                                                                 WO200112659-A2
                                                                                                                                                                                                                                                    18-AUG-1999;
28-SEP-1999;
                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       Wiemann S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173
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                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
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ABP69116
2×4×4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for Synthesising the full length cDNA are useful length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length not ferm part of the invention. Note: The sequence data for this patent did format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 IAIHEVFENSSKIVIVMEYASRGDLYDYISERQQLSEREARHFFRQIVSAVHYCHQNRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 HRDLKLENILLDANGNIKIADFGLSNLYHOGKFLOTFCGSPLYASPEIVNGKPYTGPEVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFROIVSALHYCHONGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                          Kawai Y;
T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID NO 2919; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                            Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S,
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1293; DB 4;
Pred. No. 6.5e-133;
6; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.3%;
                                                                                                                                 07-JUL-2000; 2000EP-00114089
                                                                                                                                                                        99JP-00194486
                                                                                                                                                                                       11-JAN-2000; 2000JP-00118774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   in genetic manipulation.
                                                                                                                                                                                                                                                    (HELI-) HELIX RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAK94280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 628 AA;
                  Homo sapiens
                                                     EP1130094-A2
                                                                                                                                                                      08-JUL-1999;
                                                                                            05-SEP-2001
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Matches

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RESULT 4 ABU53319

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SWSLGVLLYILVHGTMPFDGHDHKILVKQISNGAYREPFKPSDAGGLIRWLLMVPTRRA 292

SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA

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multiple sclerosis; dilabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antibarkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
                                   Human; genome mapping; gene therapy; food supplement; virus; fungus;
cell-proliferative disorder; neurodegenerative disease; bacterial;
Parkinson's disease; Alzheimer's disease; autoimmune disease;
                                                                                                                                                                                                                                                                                                      Zhao QA, Ro
, Ghosh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; SEQ ID NO 1163; 1012pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                oodrich RW, Asundi V, Zhang J, Zl
Y, Yamazaki V, Chen R, Wang Z,
Wang D, Drmanac RT;
           ID NO 1163
                                                                                                                                                                                                                                                                                                    Goodrich RW,
Ma Y, Yamaza
                                                                                                                                                                                                                           05-MAR-2002; 2002WO-US005095.
                                                                                                                                                                                                                                                     05-MAR-2001; 2001US-00,799451.
                                                                                                                                                                                                                                                                                                                                                                                                                                  coagulation disorders.
          polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from WIPO at
                                                                                                                                                                                                                                                                                                                  Æ
                                                                                                                                                                                                                                                                                                  Tang YT, Zhou P, G
Xue AJ, Yang Y, Ma
Wehrman T, Wang J,
                                                                                                                                                                                                                                                                                                                                                        2002-759812/82
                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-759812/
N-PSDB; ABZ11333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 628 AA;
                                                                                                                                                                          WO200270539-A2
                                                                                                                                                    Homo gapiens.
                                                                                                                                                                                                     12-SEP-2002
          Human
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for

Use of modulators of activity of 3700 protein for making medicament 9e.g., modulating protein phosphorylation or cell signaling, or for treating or preventing cellular proliferative and/or differentiative

Claim 19; Fig 1; 115pp; English.

disorders.

Human, protein kinase 3700, PK; protein phosphorylation, tumourigenesis, cell signalling; mitogenesis; gene transcription; angiogenesis; sarcoma; tissue repair, tissue regeneration, atherosclerosis; blood-brain barrier; cell proliferation disorder; cell differentiation disorder; carcinoma; haematopoietic neoplastic disorder; metastatic disorder; leukaemia;

AAU79652 standard; protein; 628 AA.

AAU79652 ID AAU7 RESULT 6

(first entry)

02-JUL-2002

AAU79652;

Human protein kinase 3700

TLEDVASHWWVNW 305 241 TLEDVASHWWVNW 253

В

cytostatic; antiatherosclerotic; enzyme

Ren F;

25-SEP-2001; 2001WO-US030115. 25-SEP-2000; 2000US-0234922P. (MILL-) MILLENNIUM PHARM INC.

WO200224921-A2

28-MAR-2002

Curtis RAJ, Galvin KM; WPI; 2002-352007/38 N-PSDB; ABK14000

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The invention relates to an isolated polynuclectide (I) comprising a nuclectide sequence selected from any of 948 sequences (ABZ11119-ABZ1066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynuclectides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABR68902-ABR68949) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cellimaging, atthemet's disease, autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Noce: The sequence data for this patent did not form part of the printed appecification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            !cation, but was obtained in electronic format
!ftp.wipo.int/pub/published_pct_sequences
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95.7%; Pred. No. 6.5e-133;
1ve 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 242; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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The present invention relates to the isolation of a novel human protein kinase designated 3700, and the polynucleotide sequence encoding it. The invention also describes the use of a modulator of the activity of protein kinase (PK) 3700 for making a medicament or pharmaceutical composition for modulating the ability of a cell to phosphorylate an amino acid residue of a substrate protein Modulators of protein kinase of any cell for modulating protein phosphorylation, cell angiogenesis, tissue repair, tissue repearation, establishment or progression of atherosclerosis, and signalling across the blood-brain progression of atherosclerosis, and signalling across the blood-brain parrier. The polynucleotide and polypeptide molecules for protein kinase 3700 may be used as diagnostic targets and therapeutic agents for prognosticating, diagnosing, preventing, inhibiting, alleviating, or prognosticating, disonedres (e.g. haematopoietic neoplastic disorders, carcinoma, sarcoma, metastatic disorders or leukaemia). The 3700 polynucleotide sequence can be used to express protein kinase 3700, to detect a genetic alteration in a 3700 gene, in chromosome mapping, for tissue typing, in forensic biology, and as surrogate markers. The present
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1 YEPLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI

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g 8

Sequence 628 AA;

HRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVD 232 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180

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                                                                                                                                           HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic
                                                                                                                                                                                                         1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
                                                                                 53 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New PRO polypeptides, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor adifferentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.
96.3%; Score 1293; DB 5; Length 628;
.larity 95.7%; Pred. No. 6.5e-133;
Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jackman JK, Schoenfeld JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted and transmembrane protein SeqID 640.
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                                                                                                                                                                                                                                                                                                                                                                                                                         ADF76965 standard; protein; 628
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, Wu TD;
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                al Similarity
242; Conserv
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   Query Match
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factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the CDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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method.
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1293; DB 7;
Pred. No. 6.5e-133;
6; Mismatches 5;
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2000JP-00183865.
2000EP-00114089.
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Best Local Similarity 95.7
Matches 242; Conservative
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02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
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11D ADL30886

XX AC ADL3

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PR 02-1

PR 03-1

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                                                                                               This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential theraspeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins in the sesociated with signal transduction, encoding proteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polypeptide sequence is a full length human protein of the invention.
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                                                                                                                                                                                                                                                                                                    YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
                                                                                                                                                                                                                                                                              Gaps
                                     primers (830 cDNAs) useful for synthesizing full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic, Neuroprotective, Nootropic, Muscular, Gene therapy, Adenosine Monophosphate activated Protein Kinase-related kinase 5, AMPK-related kinase 5, AMR5, KIAA0537; stress resistance, tumour, nervous disorder, muscle disorder; ataxia teleangiectasia; SNARK.
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                                                                                                                                                                                                                                                    Length 628;
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                                                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                                                                   Score 1293; DB 8;
Pred. No. 6.5e-133;
6; Mismatches 5;
                                                                          Example 1; SEQ ID NO 2919; 1340pp; English
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(PHAR-) ORG PHARM SAFETY & RES.
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                                                                                                                                                                                                                                                    96.3%;
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Best Local Similarity 95.77
Watches 242; Conservative
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 WPI; 2004-204755/20.
                                    New oligonucleotide
length human cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
           N-PSDB, ADL30885
                                                                                                                                                                                                                            Sequence 628 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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The present invention relates to human Adenosine Monophosphate activated Protein Kinase (AMPK)-related kinase 5 (ARK5/ KIAA0537) and its coding sequence, which are useful for imparting stress resistance to cells. ARK5 is useful for treatment and prevention of tumours, nervous disorders, muscle disorders and ataxia telebanglectasia. The present sequence was used to illustrate the invention.
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                                                                                             Agent for imparting stress resistance to cells, comprises DNA encoding for adenosine monophosphate activated protein kinase-related kinase 5 itreatment of tumors, muscle and nervous disorders, and ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic, cardiant, hypotensive, antianginal, osteopathic, antiarthritic, antirheumatory, antiatic, antiasthmatic, cardiovascular, virucide, analgesic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.3%; Score 1293; DB 8; Length 628; 95.7%; Pred. No. 6.5e-133; tive 6; Mismatches 5; Indels
                                                                                                                                                                                                                             Example 1; SEQ ID NO 12; 143pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human gene 3700 encoded protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLEDVASHWWVNW 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.7
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLEDVASHWWVNW
Suzuki A;
                                                  WPI; 2004-248195/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 628 AA;
                                                                                                                                                                               teleangiectasia.
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New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecules and proteins, useful for treating, e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes an isolated 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (1) comprising any one of 40 nucleotide sequences (1). The nucleic acid molecules and polypeptides are useful for diagnosing and treating a subject having a disorder, or a subject at risk of developing a disorder, which is
multiple sclerosis; Crohn's disease; psoriasis; asthma;
cell proliferation; cell differentiation; cell growth; cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rudolph-Owen LA;
Chun M, Williamson MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meyers RE,
Galvin KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 44; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kapeller-Libermann R, Hunter JJ,
Curtis RAJ, Olandt PJ, Tsai F,
Silos-Santiago I, Bandaru R;
                                                                                                                                                                                                                                        2000US-018660FP

2000US-020668P

2000US-0205447P

2000US-021925P

2000US-0234922P

2000US-0234922P

2000US-0234928P

2000US-024669P

2000US-024669P

2000US-0248893P

2000US-0248893P

2000US-0257511P

2000US-0257511P

2000US-0257511P

2000US-0260FP

2000US-0260FP

2000US-0260FP

2001US-00845644
                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-2001; 2001US-00928531.
14-AUG-2001; 2001US-00929218.
15-AUG-2001; 2001US-0312539P.
25-SEP-2001; 2001US-00963159.
08-NOV-2001; 2001US-0006016.
                                                                                                                                                                                                                  99US-00412210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2002; 2002US-00060763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001US-00003690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JAN-2003; 2003US-00336489
03-JAN-2003; 2003US-00336153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                             2003US-00423543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADL14160, ADL14162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heart failure and angina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-268788/25
                                                                          US2004058355-A1.
                                                                                                                                                                                                                                                                                                                                                         14-NOV-2000; 2
15-NOV-2000; 2
22-DEC-2000; 2
                                                                                                                                                                                                                                                                                                                    25-SEP-2000; 2
08-NOV-2000; 2
09-NOV-2000; 3
                                                                                                                                                                                                                                                                                             -JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2001;
27-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-2001;
31-JUL-2001;
                                                   Homo sapiens,
                                                                                                                             25-APR-2003;
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30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-NOV-2001;
                                                                                                   25-MAR-2004
                          human.
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assection accorder, 2644, 26649, 18093, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 SWSLGVLLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDACGLIRWLLMVNFTRRA 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention. Note: The sequences given in the specification are also avaialable in electronic format from ftp. seqdata.uspto.gov/sequence.html?DocID=2004058355.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AD020172 standard; protein; 628 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.7
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 628 AA;
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cardiovascular disease; brain; neuronal associated disease; metabolic; inflammatory disorder; cytostatic; neuroprotective; immunomodulator; antiinflammatory; enzyme; calcium/calmodulin-dependent protein Kinase; NuaK2.
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                                                                                                                                                                                                                                                      Caenepeel
                                                                                                                                                                      15-JUL-2003; 2003WO-US021730
                                                                                                                                                                                                15-JUL-2002; 2002US-0395632P.
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                                                                                                                                                                                                                                                                                 WPI; 2004-122753/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 242; Conserv
                                                                                                                                                                                                                           (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                                                            N-PSDB; ADJ96554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 672 AA;
                                                                                                                  WO2004006838-A2
                                                                             sapiens
                                                                                                                                            22-JAN-2004
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                                                                             Ношо
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ID AAE1
                                                                                        72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAIHEVPENSSKIVIVMEYASRGDLYDYISERQQLSEREARHFFRQIVSAVHYCHQNRVV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSFLYASFEIVNGKPYVGPEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HRDLKLENILLLDANGNIKTADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWSLGVLLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 292
                                                                                                                                                                                            Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human calcium/calmodulin-dependent protein kinase NuaK2 protein SeqID 77,
                                                                                                                                                                                                                                                                                     The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogran's syndrome, vasculitis, sarchidosis, autoimmune themolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, duillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy, polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kinase; human; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
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                                                                                                                  М.
                                                                                                                Schoenfeld J, Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.3%; Score 1293; DB 8; Length 628;
.larity 95.7%; Pred. No. 6.5e-133;
Conservative 6; Mismatches 5; Indels (
                                                                                                                                                                                                                                                             Claim 7; SEQ ID NO 1080; 1731pp; English.
                                                                                                                Chiu H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ96620 standard; protein; 672 AA.
                                                                                                             Dennis K, Clark H, Wu TD;
                                06-NOV-2003; 2003WO-US035268
                                                           08-NOV-2002; 2002US-0425235P
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                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                       spondyloarthropathy.
                                                                                                                                                     WPI; 2004-420067/39.
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Matches 242; Conserv
                                                                                                                                                                    N-PSDB; ADO20171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 628 AA;
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                                                                                                               Fong S, I
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This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (FTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory
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New nucleic acid molecule encoding a kinase polypeptide, useful for preparing a composition for treating diseases or disorders, e.g., cancer, or neurological, immunological or inflammatory disorders.
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Pred. No. 7.2e-133;
6; Mismatches 5;
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Human; kinase; PKIN-12; cancer; leukaemia; adenocarcinoma; osteoporosis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; ALDS, Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mallitus; osteoarthritis; Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; heparitis; hypothyroidism; cerebral palsy; cataract; angina pectoris; cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; congestive heart failure; ischemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy.
                                           Human kinase PKIN-12 protein.
                           (first entry)
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                                                                                                                                                                                                          . 269
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/note=
                           26-MAR-2002
                                                                                                                                                                             Homo sapiens
        AAE16266;
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"Eukaryotic protein kinase domain" 23. .260 /label= Protein_kinase_domain 24. .260 /label= Protein_kinase_domain /label= Protein_kinase_domain Location/Qualifiers Domain

15-JUN-2000; 2000US-0212073P.
23-JUN-2000; 2000US-0213467P.
30-JUN-2000; 2000US-0215651P.
07-JUL-2000; 2000US-021665P.
13-JUL-2000; 2000US-0218372P.
25-AUG-2000; 2000US-0228056P. 14-JUN-2001; 2001WO-US019444 WO200196547-A2 20-DEC-2001

Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y; Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR; Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT; Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R; Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L; Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH; (INCY-) INCYTE GENOMICS INC.

WPI; 2002-090207/12. N-PSDB; AAD26459 New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.

Claim 1; Page 152-153; 197pp; English

The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition containing PKIN agonist is useful for treating a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, myeloma, sarcoma, texatocarcinoma, Hodgkin's disease); immune disorder (Acquired Immune Deficiency Syndrome (ADS), asthma, Addison's disease, atheroselerosis, anaemia, allergies, adult tespitatory distress syndrome, autoimmune thyroiditis, gout, bronchitis, (Crohn's disease, diabetes mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,

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rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis, bacterial, parasitic, fungal, viral, protocoal and helminthic infections) growth and development disorders (arteriosclerosis, cirrhosis, hepatitis, cushing's syndrome, hypothyroidism, cerebral palsy, cataracts), cardio vascular disease (arteriovenous fistula, hypothemsion, vascultis, aneurysms, congestive heart fallure, angina pectoris, myocardicis, ischaemic heart disease, chronic bronchitis, lung tumours); lipid disorder (fatty liver, Rabry's disease, Namann-Pick's disease, hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity of a test compound and in gene therapy. The present sequence is human
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                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.3
Matches 241; Conservative
                                                                                                                                                                                                                                                                 Sequence 594 AA;
                                                                                                                                                                                                                      PKIN-12 protein
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ABP96085 standard; protein; 611 07-MAY-2003 (first entry) ABP96085;

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Human protein kinase SEQ ID NO:76.

Human; protein kinase; enzyme; antiasthmatic; antiinflammatory; antidabetic; antiparkinsonian; antimizabetic; cardiant; cytostatic; immunosuppressive; vulnerary; gene therapy; COPD; asthma; migraine; chronic obstructive pulmonary disease; non-insulin dependent diabetes; Parkinson's disease; myocardial infarction; inflammatory bowel disease; autoimmune disorder; allograft rejection; inflammatory bowel disease; cancer; leukaemia; wound granulation.

Homo sapiens

WO2003000901-A2

03-JAN-2003

24-JUN-2002; 2002WO-IB002358

26-JUN-2001; 2001US-0301098P 06-NOV-2001; 2001US-0332870P

(DECO-) DECODE GENETICS EHF.

Sigurdsson GT Martinez RAM,

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ABZ77126 to ABZ77165 encode the human protein kinases given in ABP96048 to ABP86087. The protein kinases have antiasthmatic, antiniflammatory, antidabetic, antiparkinsonian, antimigrafine, cardiant, cytostatic, immunosuppressive and vulnerary activities, and can be used in gene therapy. A protein kinase therapeutic agent from the present invention, particularly a protein kinase gene agonist or antagonist, can be used for treating a disease or condition associated with a protein kinase in an individual. These diseases include chronic obstructive pulmonary diseases (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease, migraine, myocardial infarction, inflammatory bowel disease, autoimmune disorders (e.g. allograft rejection or graft vs. host disease), cancers (e.g. leukaemias) or wound granulation
                                                                                                                           New protein kinase genes and polypeptides, useful for diagnosing diseases associated with a protein kinase, or in gene therapy for treating e.g. Parkinson's disease, migraine, myocardial infarction, allograft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 87; 258pp; English
N-PSDB; ABZ77163
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Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease,

neurodegenerative diseases and/or cancers

Claim 10; Fig 1; 310pp; English

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Sudersanam S;

Whyte D,

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Martinez

Plowman GD,

(SUGE-) SUGEN 28-MAY-1999;

WPI; 2001-032161/04. N-PSDB; AAF44659.

26-MAY-2000; 2000WO-US014842.

99US-0136503P

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YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI 112
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                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                          95.3%; Score 1279.5; DB 6
93.1%; Pred. No. 1.9e-131;
ive 6; Mismatches 5;
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The present sequence is a novel protein kinase. The novel protein kinases, the and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as INA probes in diagnostic assays. The kinase expression and activity. Diseases related to kinase antibodies and kinase antagonists may also be used to down regulate kinase antibodies of kinase expression and activity. Diseases related to kinase expression and activity. Diseases related to kinase autoimmune disorders, candingopopthies, strokes, renal failure, oxidative-call manner disorders, cardiomyopathies, strokes, renal failure, oxidative-call manner disorders cardiomyopathies, strokes, renal failure, oxidative-call manner and reproductive inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, processis, rhinitis, rhinitis, autoimmunity, diabetes, cancers and reproductive

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protein kinase, SEQ ID NO: 159.
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AAB65632 standard; protein; 629
               (first entry)
               27-MAR-2001
       AAB65632;
                       Novel
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Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive, cardiant, renal; antiinflammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.

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40200073469-A2
                           07-DEC-2000
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Homo sapiens

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Search completed: January 22, 2005, 06:38:27
Job time : 64.8224 secs
293 ATLEDVASHWWVNW 306
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240 ATLEDVASHWWVNW 253

181 SWSLGVLLYILVHGTWPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRR 239

233 SWSLGVLLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRR 292

HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180 173 HRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVD 232

121

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IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 120

YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI 1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI

112

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94.5%; Score 1268.5; DB 4; Length 629; ilarity 94.5%; Pred. No. 3.3e-130; Conservative 6; Mismatches 7; Indels 1;

Local Similarity les 240; Conserv

Query Match Best Loca Matches

Sequence 629 AA;

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January 22, 2005, 06:43:09; Search time 58.6708 Seconds (without alignments) 1557.950 Million cell updates/sec
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1 YEFLETLGKGTYGKVKKARE........VNPTRRATLEDVASHWWVNW 253
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1: \cgn2_6/ptodata/1/pubpaa/PCT_PBECOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 11, Appl	Sequence 103, App	Sequence 41, Appl	Sequence 50, Appl	Sequence 2, Appli	Sequence 44, Appl	Sequence 640, App	Sequence 77, Appl	Sequence 12, Appl	Sequence 101, App	Sequence 23, Appl	Sequence 26, Appl	Sequence 2, Appli
	DI	4 US-10-355-975-11	US-10-343-514-103	US-10-343-514-41	US-10-343-514-50	US-09-963-159-2	US-10-423-543-44	US-10-370-715B-640	US-10-618-941-77	US-10-311-034-12	US-10-343-514-101	US-10-322-281-23	US-10-322-281-26	US-09-780-949-2
	DB	14	16	16	16	σ	15	17	17	15	16	16	16	6
	Match Length DB ID	631	251	630	251	628	628	628	672	594	251	640	616	661
*	Match	100.0	98.7	97.8	96.6	96.3	96.3	96.3	96.3	95.8	95.1	94.9	91.7	84.1
	Score	1342	1325	1313	1296	1293	1293	1293	1293	1286	1276	1273	1230	1128.5
1 [1100]	No.	1	7	٣	4	S	9	7	œ	σ	10	11	12	13

Sequence 6, Appli Sequence 82, Appl Sequence 2553, Ap Sequence 102, App Sequence 20, Appl Sequence 29, Appl	2 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1242770444	4	
	US-10-016-248-24 US-10-016-248-71 US-10-016-248-71 US-10-016-248-70 US-10-276-645-8 US-10-016-248-70 US-09-835-081-2 US-10-258-106-16	15 US-10-276-645-7 15 US-10-363-616-403 17 US-10-425-114-54516 17 US-10-618-941-79 18 US-10-016-248-73 19 US-10-10-645-6 14 US-10-161-565-28 14 US-10-161-565-29 15 US-10-276-645-6	US-09-035-001- US-10-15-101 US-10-155-101 US-10-161-565 US-09-919-585- US-09-919-585- US-10-274-194 US-10-760-407 US-10-195-101	
661 661 252 530 246	508 639 639 752 752	752 752 752 639 660 688 724	7 7 2 2 3 4 4 7 7 2 2 3 4 4 7 2 2 2 2 4 4 5 4 5 4 5 5 5 5 5 5 5 5 5 5	
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ALIGNMENTS

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Best Local Similarity 100.0%; Pred. No. 9.4e-100;
Matches 253; Conservative 0; Mismatches 0; Indels 0;
                                                                  APPLICANT: Immunex Corporation
APPLICANT: Immunex Corporation
APPLICANT: Bird, Timothy A.
APPLICANT: Virca, G. Duke
APPLICANT: Wartin, Unja
APPLICANT: Martin, Unja
APPLICANT: Anderson, Dirk M.
ITILE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-A
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US/10/355,975
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
SOOTHWARE: Patentin version 3.1
                 Sequence 11, Application US/10355975; Publication No. US20030162277A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus US-10-355-975-11
US-10-355-975-11
                                                                                                                                                                                                                                                                                                                    SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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; TYPE: PRT
; ORGANISM: RAT
US-10-343-514-41
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                                                                                                                                                                                                                                                                                           Sequence 103, Application US/10343514

Publication No. US20040132025A1

Publication No. US20040132025A1

Sequence 103, Application Sequence 103, Publication No. US20040132025A1

APPLICANT: NOSEN, Cheryl F.

APPLICANT: ROSEN, Cheryl F.

APPLICANT: LEFEBVRE, Daniel J.

APPLICANT: APPLICANTON AMPREE: US.

TITLE OF INVENTION AMPREE: US.

CURRENT APPLICATION NUMBER: US.

CURRENT PILING DATE: 2003-01-31

PRIOR APPLICATION NUMBER: US. 60/224,650

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 109

SOFTWARE: PATCHTIN VERSION 3.0

SOFTWARE: PATCHTIN VERSION 3.0

SOFTWARE: PATCHTIN VERSION 3.0
                         181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
                                                                                                    237 SWSLGVLLYILVHGTWPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 296
121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 41, Application US/10343514
Publication No. US20040132025A1
GENERAL INFORMATION:
APPLICANT: DRUCKER, Daniel J.
APPLICANT: ROSEN, Cheryl F.
                                                                                                                                                                                      241 TLEDVASHWWVNW 253
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US-10-343-514-103
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US-10-343-514-41
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APPLICANT: LEFEBVRE, Diana L.

TITLE OF INVENTION: AMPK.RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REFERENCE: DPA-DRUGZ/PCT
CURRENT APPLICATION NUMBER: US/10/343,514

CURRENT FILING DATE: 2003-01-31

PRIOR APPLICATION NUMBER: US 60/222,650

PRIOR PILING DATE: 2001-08-08

PRIOR FILING DATE: 2001-08-08

PRIOR FILING DATE: 2001-03-12

PRIOR PILING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: US 60/274,613

PRIOR PILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 109

SOFTWARE: PALENTIN VERSION 3.0

SEQ ID NO 41

LENGTH: 630
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Publication No. US20040132025A1

GENERAL INFORMATION:
APPLICANT: DRUCKER, Daniel J.
APPLICANT: ROSEN, Cheryl F.
APPLICANT: LEFEBVER, Daniel J.
APPLICANT: LOSEN, Cheryl F.
CURRENT FILING DATE: 2003-01-31
FRIOR APPLICATION NUMBER: US/10/343,514
CURRENT FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/274,613
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 109
SEQ ID NO 50
LENGTH: 251
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Pred. No. 2e-97;
3; Mismatches 2; Indels 0
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Best Local Similarity 98.0%;
Matches 248; Conservative
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; ORGANISM: RAT
US-10-343-514-50
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US-09-963-159-2
US-09-963-159-2
; Sequence 2, Application US/09963159
; Patent No. US20020077312A1
; GENERAL INFORMATION:
; APPLICANT: Cutris, Rory A.J.
; APPLICANT: Calvin, Retherine M.
; TITLE OF INVENTION: 3700, A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR
; FILE REFERENCE: 10147-5011
; CURRENT APPLICATION NUMBER: US/09/963,159
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/234,922
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO S: 3
; SEQ ID NO S: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISSGAYREPCKPSDACGLIRWLLMVNPTRRA 240
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 Length 251;
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                               Indels
96.6%; Score 1296; DB 16;
98.0%; Pred. No. 1.7e-96;
iive 3; Mismatches 2;
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Query Match
Best Local Similarity 98.0
Matches 246; Conservative
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TYPE: PRT
CRGANISM: Homo sapiens
US-09-963-159-2
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; Sequence 44, Application US/10423543; Publication No. US20040058355A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens
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GRETHER, Megan
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LAL, Preeti
                     TYPE: PRT
CRGANISM: Homo sapiens
US-10-618-941-77
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      LENGTH: 672
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APPLICANT: BODARY, SARAH C.

APPLICANT: BLARK, HILLARY

APPLICANT: GLARK, HILLARY

APPLICANT: JACKMAN, JANET

APPLICANT: JACKMAN, JANET

APPLICANT: WILLIAMS, P. MICKEY

APPLICANT: WILLIAMS, P. MICKEY

APPLICANT: WILLIAMS, P. MICKEY

APPLICANT: WILLIAMS, P. MICKEY

APPLICANT: WILLIAMS, D. MICKEY

CURRENT APPLICATION NUMBER: US/10/370,715B

CURRENT FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 742

SEQ ID NO 640

LENGTH: 628
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Pred. No. 8.4e-96;
6; Mismatches 5; Indels 0
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Sequence 77, Application US/10618941
Bublication No. US20040197792A1
GENERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERAED
APPLICANT: CARENPEEL, SEAN
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT FILING DATE: 2003-07-15
FRIOR APPLICATION NUMBER: 60/395,632
PRIOR PRING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.2
                                                                                                                                       Sequence 640, Application US/10370715B Publication No. US20040258678A1 GENERAL INFORMATION:
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241 TLEDVASHWWVNW 253
                         241 TLEDVASHWWVNW 253
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Best Local Similarity 95.7
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-640
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                                                                                                              97 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI
                                                                                    1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
                                             Gaps
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Length 672;
                                           IndelB
Score 1293; DB 17;
Pred. No. 9e-96;
6; Mismatches 5;
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Publication No. US20040023242A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LU, Yan
GANDHI, Ameena R.
TRIBOULEY, Catherine M
CHAWLA, Narinder K.
YAO, Monique G.
LU, Dyung Aina M.
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APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, SAJERV
APPLICANT: ISON, CRAIGH.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
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GURURAJAN, Rajagopal
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GRIFFIN, Jennifer A
KEARNEY, Liam
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POLICKY, Jennifer L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHAH, Farrah A.
RECIPON, Shirley A.
Query Match
Best Local Similarity 95.7%;
Matches 242; Conservative
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BOROWSKY, Mark L.
AU-YOUNG, Janice
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TANG, Y. Tom
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THORNTON, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLY--DEIVNGKPYVGPEVD
                                                    1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI
                                                                                                       IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHONGIV
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                           1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
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Publication No. US20040126/62A1

GENERAL INFORMATION:

JAPLICANT: David W. Morris

APPLICANT: Marc S. Malandro

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

FILE REFERENCE 5.29452001000

CURRENT APPLICATION NUMBER: US/10/322,281

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 866

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 640
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APPLICANT: David W. Morris; APPLICANT: Marc S. Malandro
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, ORGANISM: Mus musculus
US-10-322-281-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-10-322-281-23
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US-10-322-281-26
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                                                                             PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-07 NUMBER OF SEQ ID NOS: 52 SOFTWARE: PERL Program SEQ ID NO 1.2 LENGTH: 594
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
CURRENT FILING DATE: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372; 60/228,056
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publication No. US20040132025A1

publication No. US20040132025A1

publication No. US20040132025A1

APPLICANT: ENCERN, Daniel J.

APPLICANT: ROSEN, Cheryl F.

APPLICANT: LEFEBVRE, Diana L.

TILE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK

FILE REFERENCE: DPA-DRUCZ/PCT

CURRENT APPLICATION NUMBER: US/10/343,514

CURRENT APPLICATION NUMBER: US/10/313

PRIOR FILING DATE: 2001-08-02

PRIOR PELING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 109

SEQ ID NO 101

LENGTH 251

TENGTH 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.1%; Score 1276; DB 16; Length 251; 95.6%; Pred. No. 7.2e-95; ive 6; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                 ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 4841542CD1
US-10-311-034-12
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Best Local Similarity 95.6
Matches 240; Conservative
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60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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                                                                                 180 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR
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                                                              180 DSWSLGVLLYILVHCTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR
                                                                                                                                                                                                                                                              Sequence 6, Application US/09780949
; Sequence 6, Application US/09780949
; Patent No. US20020006618A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liberman, Rosana
APPLICANT: Weich, Nadine 8.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: Methods for Using 20893, a Human Protein
; TITLE OF INVENTION: Methods for Using 20893, a Human Protein
; TITLE OF INVENTION: Minase
; TITLE OF INVENTION: Minase: US/09/780,949
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LUNGTH: 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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84.1%; Score 1128.5; DB 9; Length 661;
Best Local Similarity 82.3%; Pred. No. 1.6e-82;
Matches 209; Conservative 24; Mismatches 20; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Hunter, John Joseph
APPLICANT: MacBeth, Kyle J.
APPLICANT: Tsai, Fong-Ying
APPLICANT: Lesoon, Andrea
APPLICANT: Lightcap, Eric S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 82, Application US/10354358 Publication No. US20030157082A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rudolph-Owen, Laura A.
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ATIEDIANHWWVNW 308
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295 ATIEDIANHWWVNW 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: H. sapiens
US-09-780-949-6
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US-09-780-949-6
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                              53 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI 112
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Patent No. US2002006618A1

GENERAL INFORMATION

APPLICANT: Kapeller-Liberman, Rosana

APPLICANT: Galvin, Katherine M.

TITLE OF INVENTION: Minase

FILE REPERENCE: 035800/209015

CURRENT APPLICATION NUMBER: US/09/780,949

CURRENT FILING DATE: 2001-02-09

PRIOR FILING DATE: 2000-02-09

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 2

LENGTH: 661
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                                                                                                                                                                                                                                               Length 616;
  TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                           Score 1230; DB 16
Pred. No. 9.8e-91;
6; Mismatches 5
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Best Local Similarity 93.3
Matches 236; Conservative
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                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: H. sapiens
US-09-780-949-2
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                                                                                                                                               LENGTH: 616
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Best Local Si
Matches 209,
                                                                                                                          SEQ ID NO 26
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: TAGO. 2561, 69583
TITLE OF INVENTION: 718J, 7660, 2561, 69583, 49863, 8937, 1682, 1767, 2035,
TITLE OF INVENTION: 718J, 7660, 2561, 69583, 48964, 2088, 33427, 2160,
TITLE OF INVENTION: 9252, 9389, 1642, 86289, 10597, 1564, 9953,
TITLE OF INVENTION: 9392, 2100, 2388, 1660, 1680, 20893, 33429, 2166,
TITLE OF INVENTION: 9392, 2100, 2888, 10480, 20893, 33429, 1686, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32256, 2099,
TITLE OF INVENTION: 2160, 26583, 2744, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
TITLE OF INVENTION: 2002-0130, 2003-1013, 6108
TITLE OF INVENTION WINNER: US 60/353,600
PRIOR PLING DATE: 2002-01-31 60/353,600
PRIOR PLING DATE: 2002-01-31 60/353,600
PRIOR PLING DATE: 2002-01-31 60/371,075
PRIOR PLING DATE: 2002-01-31 60/371,075
PRIOR PLING DATE: 2002-04-10
PRIOR PLING DATE: 2002-06-10
PRIOR PLING DATE: 2002-06-17
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82.3%; Pred. No. 1.6e-82;
ive 24; Mismatches 20; Indels 1;
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ATIEDIANHWWVNW 308
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Best Local Similarity 82.3
Matches 209; Conservative
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ORGANISM: Homo sapiens
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January 22, 2005, 06:29:16; Search time 15.4548 Seconds (without alignments) 1575:104 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                   - protein search, using sw model
                                                                                   OM protein
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US-09-980-464-11_COPY_57_309 1342 1 YEFLETLGKGTYGKVKKARE.........VNPTRRATLEDVASHWWVNW 253 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	hypothetical prote	serine/threonine p	probable serine/th	serine/threonine-s	probable serine/th	hypothetical prote	serine/threonine-s	serine/threonine-s	probable serine/th	probable serine/th	protein H39E23.1	SNF-related kinase	serine/threonine-s	probable serine/th	qik protein - chic	hypothetical prote	FOG2 protein - yea	serine/threonine-s	[hydroxymethylglut	[hydroxymethylglut	probable serine/th	probable carbon ca	hypothetical prote	protein kinase - m	serine/threonine p	serine/threonine-s	serine/threonine-s	SNF1-related prote	serine/threonine-s
SUMMARIES	ID	T29253	G01025	S27966	T52633	T10449	T13741	JC1446	A56009	148609	T18611	G89287	B90100	A26030	T07415	JC7500	T29858	872513	S59941	S51025	A53621	T07788	T41587	T20941	149072	T04145	S44859	A41361	B90120	860303
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	Query Match Length DB	1558	745	713	512	504	1398	512	511	774	1192	1246	472	633	504	798	562	602	473	552	552	512	576	887	481	510	622	502	401	513
dю	Query Match	9.09	48.2	48.2	48.0	47.8	47.6	47.5	47.0	46.8	46.3	46.3	46.3	46.2	46.1	46.0	45.9	45.8	45.5	45.0	44.8	44.6	44.1	43.5	43.2	43.0	42.7	42.3	42.2	41.8
	Score	813.5	647.5	646.5	644	641	638.5	637	631	627.5	621.5	621.5	621	619.5	618	617.5	919	614.5	610	604	601	599	591.5	583.5	579.5	576.5	573	567.5	566.5	561.5
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RESULT 2
G01025
serine/threonine protein kinase - human
c:Species: Homo sapiens (man)
C;Date: 21-Dec.1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004
C;Accession: G01025

serine/threonine-s	protein kinase kin	protein kinase 1 -	probable protein k	p69Eq3 protein - A	probable serine/th	probable serine/th	GIN4 protein - yea	probable serine/th	serine/threonine-s	serine/threonine-s	probable protein k	probable purine nu	probable protein k	serine/threonine-s	hypothetical prote
S60304	T40503	A38903	C84667	S52244	A86427	T14735	859359	T14736	S64930	S52687	E84707	S37928	T02306	T09903	E96522
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513	891	891	441	651	480	440	1142	440	1147	1064	435	1518	502	445	421
æ	40.3	40.2	39.8	39.7	39.7	39.3	39.2	39.5	39.1	39.0	38.8	38.5	38.0	37.8	37.3
41.8	4														
560.5 41		540	534.5	533	532.5	527.5	526	525.5	525	523	521	516	510	507.5	500.5

ALIGNMENTS

RESULT 1 T29253 C;Species: C;Date: 15- C;Accession R;Murray, J Submitted th A;Reference A;Recession A;Reference A;Recession A;Residues: A;Residues: A;Residues: A;Cross-ref A;Experimen C;Genetics: A;Genetics:	RESULT 1 T29253 Hypothetical protein B0496.3 - Caenorhabditis elegans C; Secies: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C; Accession: T29253 R; Murray, J; Le, T.T. Submitted to the EMBL Data Library, May 1996 A; Description: The sequence of C. elegans cosmid B0496. A; Reference number: Z20596 A; Reference number: Z20596 A; Residues: DNA A; Residues: 1-1558 cMUR> A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-1558 cMUR> A; Residues: 1-1558 cMUR> A; Residues: 1-1558 cMUR> A; Cross-references: EMBL:U58749; PIDN:AAB00636.1; GSPDB:GN00022; CESP:B0496.3 A; Experimental source: strain Bristol N2; clone B0496 C; Genetics: CESP-80496.3 A; Map position: 4 A; Inutrons: 55/1; 100/3; 141/1; 226/3; 298/1; 468/3; 502/2; 609/3; 656/3; 795/3; 94
Best I Best I Matche Oy Oy Oy Oy Oy	Deet Local Similarity 61.7%; Score 813.5; Deb 2; Length 1558; Best Local Similarity 61.7%; Pred. No. 2.76-27; Matches 156; Conservative 33; Mismatches 63; Indels 1; Gaps 1; 1 YEFLETLGKGTYGKVKRARESS-GRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH 59
λ Q	240 ATLEDVASHWWNN 252 : 315 ATIFDIASHWWLN 327

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serine/threonine-specific protein kinase (EC 2.7.1.-) AKINI1 [validated] - Arabidopsis th
N/Alternate names: SNF1 protein kinase omolog AKINI1
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: T52633
R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machida, Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A;Title: Regulatory interaction of PRLI WD protein with Arabidopsis SNF1-like protein kin. A;Reference number: 225116; MUID:99238528; PMID:10220464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Description: EC 2.7.1.-; serine/threonine-specific protein kinase AKIN11 [validated, MC complements SNP1 mutations in yeast
C;Superfamily: AMP-activated protein kinase, protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
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A,Experimental source: cultivar Columbia
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A;Molecule type: mRNA
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S, Gumpel, N.J.
Submitted to the EMBL Data Library, December 1996
A, Reference number: 217020
A, Accession: T10449
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
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                                                                                                                               239 RATLEDVASHWWVN 252
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C;Superfamily: protein kinase homology
C;Superfamily: protein kinase homology
F;S4-307/Domain: protein kinase homology <KKI/h
F;62-70/Region: protein kinase ATP-binding motif
              R;Navarro, E.
submitted to the EMBL Data Library, April 1996
A;Reference number: H00564
A;Accession: G01025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Mcleaule type: mRMA
A;Mcsiques: 1-745 ANAV
A;Resiques: 1-745 ANAV
A;Cross-references: UNIPROT:Q15524; UNIPROT:Q96HB3; EMBL:X97630; NID:g1310674
C;Superfamily: protein kinase homology
F;18-271/Domain: protein kinase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
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48.2%; Score 646.5; DB 2; Length 713;
Best Local Similarity 51.6%; Pred. No. 1.4e-20;
Matches 131; Conservative 41; Mismatches 79; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                    Length 745;
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                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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51.2%; Pred. No. 1.3e-20;
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Best Local Similarity 51.2'
Matches 130; Conservative
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Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: J3-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
Rimurphy, L.; Harris, D.; Barrell, B.
Submitted to the EMBL Data Library, April 1999
A; Pescription: Sequencing the distal X chromosome of Drosophila melanogaster.
A; Pescription: Sequencing the distal X chromosome of Drosophila melanogaster.
A; Reference number: Z1768
A; Reference number: Z1768
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: DNA
A; Molecule type: DNA
A; Residues: UNIPROT: O77268; EMBL: ALO31765; NID: e1371523; PID: e1329905; PIDN: CAA2
A; Cross-references: FlyBase: FBgn0000667
A; Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3
A; Note: EG: 2225.8
                                              peptidyl-threonin
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                                                                                                                                                                                                                                                                                                 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
                                                                                                                                                                                                                                                                                                                       VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
                                                                                                                                                                                                                                                                                                                                                                                                  DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPK-PSDACGLIRMLLMVNPTR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 VHRDLKAENLLLDLNMNIKIADFGFSNHFKPGELLATWCGSPPYAAPEVFEGKQYTGPEI 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: cv. Masterpiece; cotyledon
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidy
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                        |: :||| |::|||| | : | |||| : ||||| 8 YKLGKTLGIGSFGKVKIAEHALTGHKVAIKILANRRKIKNLDMEEKVRREIKILRLFMHPH
                                                                                                                                                                                                                   1 YEFLETLGKGTYGKVKKARES-SGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH
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                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)
                                                                                                                                      tch 47.8%; Score 641; DB 2; Length 504; al Similarity 50.4%; Pred. No. 1.8e-20; 127; Conservative 47; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 RATLEDVASHWWV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |: :: | |
RITIPEIRQHPW 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.28 Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATLEDVASHWW 250
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                                                                                                                                      Query Match
Best Local &
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A,Molecule type: DNA
A,Residues: 144-198 <TH2>
A,Cross-references: EMBL.X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
C,Comment: This enzyme plays an important role in a signal transduction cascade regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C; Superfamily: AMP-activated protein kinase; protein kinase homology C; Superfamily: AMP-activated protein kinase; serine/threonine-specific protein kinase F; 17-271/Domain: protein kinase homology <KIN>
F; 17-271/Domain: protein kinase ATP-binding motif F; 48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted F; 147,151/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 novel protein kinase genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:9166600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase
                                                                                                                                                                                                               Serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana NiAlternate names: protein kinase SNF1 homolog (5) Species: Arabidopsis thaliana (mouse-ear cress) (5) Species: Arabidopsis thaliana (mouse-ear cress) (5) Species: Arabidopsis thaliana (mouse-ear cress) (5) Species: 30-Sep-1993 #text_change 09-Jul-2004 (5) SACCESSION: JC1446; SS8266; S66334 (8) Species: JC1446; SS8266; S66334 (8) Species: A: Thomas, M.; Blanchi, M.; Halford, N.G.; Kreis, M. A: A: Title: Structure and expression of a gene from Arabidopsis thaliana encoding a paragraphy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JC1446
A; Molecule type: DNA
A; Mesidues: 1-512 <LEGs
A; Cross = references: UNIPROT:038997; GB:M93023; NID:g166599; PIDN:AAA32736.1; PID:g
R; Thuemmler, F:; Kirchner, M.; Teuber, R.; Dittrich, P.
Submitted to the EMBL Data Library, May 1995
A; Accession: Sig256
A; Accession: Sig256
A; Accession: Sig256
A; Accession: Sig256
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 14-198 <-THU-
A; Residues: 14-198 <-THU-
A; Residues: 14-198 <-THU-
A; Coss-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
R; Thuemmler, F:; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A; Reference number: S66314; MUID:9612333; PMID:8B34852
A; Accession: S66314; MUID:96123233; PMID:8B34852
A; Accession: S66334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGIYTLPSHLSPGARDLIPRMLVVDPMK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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49.6%; Pred. No. 2.7e-20;
Live 50; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 49.6%;
Matches 125; Conservative 5
| |::: | |:
RYTIDOIKRHRWM 392
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RVTIPEIRQHPW 270
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Gaps

ë, 774;

80; 'n

Length Indels

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|::||| ::|||| ::||||| |:::||:
112 IVKLFEVIETEKTLYLVMEYASGGEVFDYLVAHGRMKEKEARAKFRQIVLHVQYCHQKFI 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKFSDAC-GLIRWLLMVNPTR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 YRLLKTIGKGNFAKVKLÆRHLTGKEVAVKIIDKTOL-NSSSLOKLFREVRIMKVLNHPN 111
                                                              C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
P;51-304/Domain: protein kinase homology <KIN>
F;59-67/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                       1 YEFLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH
                                                                                                                                                                                       Query Match
46.8%; Score 627.5; DB 2
Best Local Similarity 50.0%; Pred. No. 8.9e-20;
Matches 127; Conservative 44; Mismatches 8C
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A; Cross-references: EMBL: X70764
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                    C, Genetics:
A, Gene: emk
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A,Residues: 1-511 <MUR>
A,Residues: 1-511 <MUR>
A,Residues: 1-511 <MUR>
A,Residues: 1-511 <MUR>
C,Function: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C,Superfamily: AMP-activated protein kinase; protein kinase homology
C,Superfamily: AMP-activated protein kinase; serine/threonine-specific protein kinase
F,17-271/Domain: protein kinase homology <KIN>
F,18-331/Region: protein kinase ATP-binding motif
F,25-331/Region: protein kinase ATP-binding motif
F,48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F,147,151/Binding site: magnesium (Asn, Asp) #status predicted
                                   ASE009

serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
c;Species Nicotiana tabacum (common tobacco)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C;Accession: A56009
C;Accession: H: Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces certase of Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable serine/threonine-specific protein kinase (EC 2.7.1.-) kem - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 148609; S11333
R;Inglis, J.D.; Lee, M.; Hill, R.E.
Mamm. Genome 4, 401-403, 1993
A;Title: Emk. a protein kinase with homologs in yeast maps to mouse chromosome 19. A;Fitle: Emk. a protein kinase with homologs in yeast maps to mouse chromosome 19. A;Cession: 148609
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-774 <ING1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPS-DACGLIRWLLMVNPTR 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                    A;Reference number: A56009; MUID:94217693; PMID:8164654
A;Accession: A56009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.0%;
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Matches 125; Conservative
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probable serine/threonine-specific protein kinase (EC 2.7.1.-), long splice form - Caenoi N.Contains: probable scrine/threonine kinase, short splice form C.Species: Caenorhabditis elegam C.Species: Caenorhabditis elegam C.Species: 15-0ct-1999 #sequence revision 15-0ct-1999 #text_change 09-Jul-2004 C.Accession: T18611; T18610; T23144; T23143
                                                                                                                                                                                                                                                                                                                                                                                                       , Residues: 1-1192 <WILL>
, Cross-references: UNIPROT: Q9TW45; EMBL: Z81027; PIDN: CAB54179.1; GSPDB: GN00023; CESP: H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-487,536-1192 <WIL2>
A;Cross-references: EMBL:Z81027; PIDN:CAB54178.1; GSPDB:GN00023; CESP:H39E23.1b
A;Experimental source: clone AH10
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A.Cross-references: EMBL: Z96102; PIDN:CAB54263.1; GSPDB:GN00023; CESP:H39E23.la
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                                                                                                                                                                                                                          submitted to the EMBL Data Library, October 1996
A;Reference number: 218997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R,McMurray, A. submitted to the EMBL Data Library, June 1997 A;Reference number: 219696 A;Accession: T23144
                                                                                                                                                                                                                                                                                                  A; Accession: T18611
A; Status: translated from GB/EMBL/DDBJ
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A;Status: translated from GB/EMBL/DDBJ
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A,Cross-references: EMBL:296102;
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A;Cross-references: UNIPROT:Q05512; EMBL:X70764; NID:g57919; PIDN:CAA50040.1; PID:g57920 R;Inglis, J.D.; Lee, M.; Hill, R.E. Embl. Parary, January 1993 A;Description: A novel protein kinase with homologues in yeast maps to mouse chromosome A;Reference number: S31333

A;Molecule type: mRNA A;Residues: 1-698,'K',700-702,'GRGLPTAAKASCTSGTCYCAGMAHQATRT',731-774 <ING2>

A; Accession: S31333

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RSSLDNIMKDRWMN 312
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A; Residues: 1-633 <DIE>
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: G89287
R;Anonywous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G89287
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-1246 <STO>
A;Introns: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 487/3; 535/3; 631/1; 825/2; 914/3; 99Z (*keywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific pro F;1-1192/Product: probable serine/threonine-specific protein kinase, long splice form #6 F;1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short splide F;1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short splid
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                                                                                     Query Match 46.3%; Score 621.5; DB 2; Best Local Similarity 48.0%; Pred. No. 2.2e-19; Matches 122; Conservative 52; Mismatches 77;
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Pred. No. 2.2e-19;
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RSSLDNIMKDRWMN 422
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Best Local Similarity
Matches 122; Conserv
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A;Cross-references: UNIPROT:Q98RL9; GB:AF165818; NID:g13794554; PIDN:AAK39929.1; GSPDB:G.
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C;Date: 20-Aug-1987 #sequence_revisiae
C;Date: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 09-Jul-2004
C;Accesta, J.L.; Carlson, M.
Science 233, 1175-1180, 1986
A,Fitle: A yeast game that is essential for release from glucose repression encodes a pr. A;Reference number: A26030; MUID:86289463; PMID:3526554
A,Ression: A26030
A,Molecule type: DNA
A,Residues: 1-633 <CEL>
A,Residues: 1-633 <CEL>
R,Dietrich, F.S.
                                                                                                                                                                  Deng, L.T.; Wu, X.; Rei
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SWF-related kinase [imported] - Guillardia theta nucleomorph Gispecies: nucleomorph Guillardia theta Alfote: a nucleomorph Guillardia theta Alfote: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont Cibate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C; Accession: B90100
R;Douglas, S:; Zauner, S:; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Nature 410, 1091-1096, 2001
A;Reference number: A99082; MUID:11323671; PMID:11323671
A,Accession: B90100
A;Status: preliminary
A,Molecule type: DNA
A;Residues: 1-472 < DOU>
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C;Superfamily: AMP-activated protein kinase; protein kinase homology
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A;Description: The sequence of S. cerevisiae cosmids 9410, 8035,
A;Reference number: S69554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 472;
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48.0%; Pred. No. 1.2e-19;
tive 52; Mismatches 78
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RITINEIRDHPWFN 265
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Matches 122; Conservative
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60 IIAIHEVPENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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Best Local Similarity 48.6%
Matches 123; Conservative
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257 RISVPDIRQHQW 268
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A; Residues: 1-798 <XIA>
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NyAlternate names: SNP1-related protein kinase
C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07415
R;Halford, N.G.
submitted to the EMBL Data Library, March 1996
A;Reference number: 216022
A;Accession: T07415
A;Accession: T07415
A;Reference number: 22602
A;Reference number: 22603
A;Reference number: 22603
A;Reference number: 22604
A;Reference number: 2260/3; 2260/3; 320/3; 348/3; 389/3; 466/3
A;Genetics
A;Gen
A;Cross-references: EMBL:U33050; NID:g927726; PIDN:AAB64904.1; PID:g927732; GSPDB:GN0000 C;Genetics: A;Genetics: A;Genetics: GD:SNP1; MIPS:YDR477w
A;Cross-references: SGD:S0002885; MIPS:YDR477w
A;Cross-references: SGD:S0002885; MIPS:YDR477w
A;Description: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A;Description: catalyzes the formation of glucose-repressed genes in response to glucose depriv S;Superfamily: Awh-activated protein kinase; protein kinase homology C;Superfamily: Awh-activated protein kinase; protein kinase homology C;Reywords: ATP; autophosphorylation; magnesium; nucleus; phosphoprotein; phosphotransfe F;53-306/Domain: protein kinase ATP-binding motif F;53-306/Domain: protein kinase ATP-binding motif F;54-109/Active site: Lys, Glu. Asp, Lys #status predicted F;182,186/Binding site: magnesium (Asn, Asp) #status predicted F;220/Binding site: phosphate (Thr) (covalent) (by unidentified kinase) #status predicte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69; Indels
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48.2%; Pred. No. 1.7e-19;
tive 57; Mismatches 69
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NRISIHEIMQDDW 305
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Best Local Similarity 48.2
Matches 122; Conservative
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Best Local S:
Matches 123
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A;Cross-references: UNIPROT:Q91A88; GB:AF219232
C;Comment: This protein, a member of the AMPK/SNF1 family of serine/threonine kinases, fi
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120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
                                                                                                      180 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSD-ACGLIRWLLMVNPTR 238
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                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: Qin-induced kinase
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 YDIERTLGKGNFAVKLARHRYTKTQVAIKIIDKTRL-DPSNLEKIYREVQIMKLLNHPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rixia, Y.; Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J. Biochem. Blophys. Res. Commun. 276, 564-570, 2000
A;Title: The new serine-threonine kinase, Qik, is a target of A;Reference number: QC7500
A;Concents: Embryo fibroblasts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.0%; Score 617.5; DB 2;
48.6%; Pred. No. 2.4e-19;
tive 47; Mismatches 80;
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

January 22, 2005, 06:28:10 ; Search time 74.4118 Seconds (without alignments)

1956.274 Million cell updates/sec
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Title: US-09-980-464-11_COPY_57_309

Perfect score: 1342

Sequence: 1 YEPLETLGKGTYGKVKKARE......VNPTRRATLEDVASHWWVNW 253

Sequence: 1 YEPLETLGKGTYGKVKKARE.. Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTE

	Description	Q8cic0 mus musculu		Q80zw3 mus musculu	Q8bzn4 mus musculu	Q9h093 homo sapien	O60285 homo sapien	3 hon	Q6i6d6 mus musculu	Q7qbh4 anopheles g	Q7kss0 drosophila			Q9vh05 drosophila	м	Q8wqg7 caenorhabdi	Q9bibl caenorhabdi	Q96134 homo sapien	Q8cip4 mus musculu	Q8ng37 homo sapien	Q804t2 xenopus lae		Q9jke5 mus musculu	Q7qbh3 anopheles g	Q96rg0 homo sapien		Q6pdr4 mus musculu	Aah58556 mus muscu	homo	Q7kzi7 homo sapien	Q96hb3 homo sapien	Aah08771 homo sapi
SUMMARIES	Ħ	QBCICO	Q9DBV0	QBOZW3	Q8BZN4	О9ноэ	ARKS_HUMAN	BAA25463	Q616D6	Q7QBH4	Q7KSS0	Q7YU19	AAS65135	Q9VH05	AAF54517	Q8WQG7	Q9BIB1	MRK4_HUMAN	Q8CIP4	Q8NG37	Q804T2	Q9JKE4	Q9JKE5	070вн3	Q96RG0	008679	Q6PDR4	AAH58556	015524	Q7KZI7	096нвз	AAH08771
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	Query Match Length	631	631	639	639	628	661	698	575	383	1180	1180	1180	1427	1427	1566	1607	752	752	752	725	729	744	712	691	722	722	722	745	755	778	778
d	Query Match	100.0	100.0	99.0	99.0	96.3	84.1	84.1	76.4	61.4	61.3	61.3	61.3	61.3	61.3	9.09	9.09				48.6		48.5	•	•			•	48.2	•	48.2	48.2
	Score	1342	1342	1328	1328	~		1128.5	1025	824.5	822.5	822.5	822.5	822.5		813.5	813.5			6.099	652.5	651.5	651.5	650	647.5	647.5	647.5	647.5	647.5	47.	•	647.5
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	Q8vhf0 rattus norv	Osbr95 mus musculu	P92958 arabidopsis	P92968 arabidopsis	Q802w0 brachydanio	Ofint7 xenopus lae	Aah72186 xenopus l	O08678 rattue norv	Q8vhj5 mus musculu	Q7zyl7 xenopus lae		P93113 cucumis sat		
	QBVHF0	Q8BR95	P92958	P92968	Q802W0	Q61NT7	AAH72186	008678	QBVHJS	Q7ZYL7	Q8QGV3	P93113	075271	Q6V8Y5
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	797	888	512	512	722	792	792	793	795	176	785	504	462	542
,-	48.2	48.2	48.0	48.0	48.0	47.9	47.9	47.9	47.9	47.8	47.8	47.8	47.7	47.7
	647.5	647.5	644	644	643.5	642.5	642.5	642.5	642.5	641.5	641.5	641	640.5	640.5
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ALIGNMENTS

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FANTOM Consortium,
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200013B22 product:weakly similar to PROBABLE SERINE/THREONINE-
PROTEIN KINASE KIAAOS37 (EC 2-7.1.-) (Mus musculus adult male cecum
CDNA, RIKEN full-length enriched library, clone:9130215K18

product:weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                      1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
                                                                                                                                                                                                                                                                                                                 Gaps
               InterPro; IRR00019; Prot Kinase.
InterPro; IRR000290; Ser thr pkinase.
InterPro; IRR002290; Ser thr pkinase.
InterPro; IRR008271; Ser thr pkinase.
Probom; PR00691; Prot kinase; 1.
SMART; SM00220; STKc; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 631 AA; 69745 MW; CGC9042247D9174F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                    100.0%; Score 1342; DB 2; Length 631; 100.0%; Pred. No. 1.2e-97; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    631 AA
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STRAIN=CSTBL/61, TISSUE=Cecum, and Lung;
MEDI.NE=2108560; Pubmed=11217851;
RIKEN PANTOM CONSORTIUM;
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STRAIN=C57BL/6J; TISSUE=Cecum, and Lung;
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InterPro; IPR011009; Kinase like
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Best Local Similarity
Matches 253; Conserv
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Name=1200013B22Rik;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg E., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg E., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg E., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villaton D.K., Muzny D.W., Sodesgren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakeeley R.W., Tucchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse convasions of more convasions and processes."
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                           PROSITE; PSO0107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threomine-protein kinase; Transferase.
SEQUENCE 631 AA; 69806 MW; D51C042DE6CC174B CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                             100.0%; Score 1342; DB 2; Length 631; 100.0%; Pred. No. 1.2e-97;
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Last annotation update)
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                                                                                                                                                                                                                                                                                             0; Mismatches
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STRAIN=C57BL/6; TISSUE=Brain;
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STRAIN=C57BL/6; TISSUE=Brain;
Strausberg R.;
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253; Conservative
   SMART; SM00220; S_TKC; 1
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Name=1200013B22Rik;
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CQ80ZW3
CQ80Z
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Prodom; Protocomis Protocomes, 1.

SWART; SW000020; S.TKG; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEOUENCE 639 AA; 70675 MW; FB9C40228F53872C CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                        HSSP, P31751; 1GZK.

MGD; MGI:1921387; 1GZK.

MGD; MGI:1921387; 1200013B22Rik.

GO; GO:0004674; F:ATP binding; IEA.

GO; GO:00046740; F:protein serine/threonine kinase activity; IEA.

GO; GO:0016740; F:protein amino acid phosphorylation; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR00109; Kinase like.

InterPro; IPR002290; Ser_thr_pkinase.

InterPro; IPR008271; Ser_thr_pkinase.

InterPro; IPR008271; Ser_thr_pkinase.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annocation update)
01-MAR-2004 (TrEMBLrel Last annocation update)
Mus musculus adult male diencephalon cDNA, RIKEN full-length
library, clone:9330154N24 product:weakly similar to PROBABLE
SERINE/THERONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-).
                               family
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   the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: Belongs to the Ser/Thr protein
EMBL; BC046833; AAH46833.1; -.
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STRAIN=CS7BL/6J; TISSUE=Diencephalon;
MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Diencephalon;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Matches 253; Conservative
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Hangaki T., Hara A., Hashizume W., Furuno M., Hirancko K., Hiracka T., Hirozane T., Hayatsu M., Hirancko K., Hiracka T., Hirozane T., A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saito H., Sakai C., Sakazume N., Sano H., A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Labultted (JUL-2001) to the EmBL/GenBank/DDBJ databases.

Shila AK034082; BAC28575.1; --
                                                                                     SEQUENCE FROM N.A.
STRANIE-STBL/61; TISSUE=Diencephalon;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                  Carrinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA ibraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/61; TISSUE-Diencephalon;
MEDLINE-20530913; PubMed-11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamacto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS010109; PROTEIN KINASE Tr; 1.
ATP-binding; Kinase; Parine/threonine-protein Kinase; Transferase.
SEQUENCE 639 AA; 70632 MW; PB98EE915C95FA5D CRC64;
              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:1921387; 1200013B22Rik.
GO:0005524; F:ATP binding; IEA.
GO:0004674; F:protein serine/threonine kinase activity; IEA.
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Pred. No. 1.6e-96;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase_like.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR008371; Ser_thr_pkinase.
ProDom; PD000009; Pkinase; I.
ProDom; PD000001; Prot kinase; I.
SM00220; S_TKC; I.
                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Diencephalon;
MEDLINE=20499374; PubMed=11042159;
RIKEN FANTOM Consortium;
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MEDINEE-199825;

MEDINEE-199825;

MEDINEE-238825;

MEDINEE-238825;

MEDINEE-238825;

MEDINEE-238825;

MALEGUID E.A., Grouse L.H., Derge J.G.,

MALEGUID S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MALSCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MALSCHUL S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

MA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MA Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

MA Nilaion D.K., Muzny D.M., Soderjen B.J., Lu X., Gibbs R.A.,

Milaion D.K., Muzny D.M., Soderjen B.J., Lu X., Gibbs R.A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makealey R.W., Touchman J.W., Green B.D., Dickson M.C.,

Markealey R.W., Touchman J.W., Garen B.D., Dickson M.C.,

Markealey R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,

Markealey M., Matan M., Young M. Smailus D.E., Schnerch A., Schein J.E.,

Markealey R.W., Markea M.A.,

Mannes S.J., Mannes S.J., Markea M.B.,

Mannes S.J., Markea M.A.,

Mannes S.J., Markea M.J.,

Mannes S.J., Markea M.J.,

Mannes S.J., Markea M.J.,

Mannes S.J., Mannes S.J.,

Mannes S.J., Markea M.J.,

Mannes S.J., Markea M.J.,

Mannes S.J., Markea M.J.,

Mannes S.J., Markea M.J.,

Mannes 
                              57 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIBIMSSLNHPHI 116
                                                                                                                                   113 YCHQNGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGK 172
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                                                                                                        IAIHE------VFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALH 112
9
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Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKPZp434J037 (Hypothetical protein SNARK)
(Hypothetical protein FLJ90349).
Name=DKFZp434J037, Synonyms=SNARK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Testis;
Koehrer K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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Query Match
Best Local Similarity 96.9%;
Matches 253; Conservative

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code for large proteins in vitro.
MA Res. 5:31-39(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
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A Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
A Mamanoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
A Mathor Y., Ono T., Okano K., Yoshikwa Y., Aotauka S., Sagaki N.,
A Hattori A., Okumura K., Iwayanagi T., Ninomiya K.,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
I. Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL136891; CAB6682.1; -
EMBL; AL136891; CAB6682.1; -
R EMBL; AK07480; BAC11234.1; -
R GO; GO:0006524; F:ATP binding; IEA.
GO; GO:0006524; F:ATP binding; IEA.
GO; GO:0016740; F:protein merino acid phosphorylation; IEA.
R GO; GO:0006468; P:protein maino acid phosphorylation; IEA.
InterPro; IPR001109; Kinase like.
InterPro; IPR002290; Frot Kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Frot Kinase.
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Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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95.7%; Pred. No. 9.3e-94;
ive 6; Mismatches 5; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
AMPL-related protein kinase 5 (EC 2.7.1.37).
Name-ARK5; Synonyms=KIAA0537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
ATP-binding; Hypothetical protein; Kinase;
Serine/threonine-protein kinase; Transferase.
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060285;
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EMBL; ABOULLO9; bc.

HSSP; P31751; 1GZK.

MIM; 608130; ...

R InterPro; IPR000719; Prot Kinase.

DR InterPro; IPR000719; Prot Kinase.

DR PROSITE; PS00100; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE T; 1.

KW ATP-binding; Phosphorylation; Polymorphism; KW Serinc/threonine-protein kinase; Transferase.

DOMAIN 61 69 ATP (By similarity).

R 178 178 PROFON SECEPTOR (By similarity).

PTOTO ACCEPTOR (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 VHRDLKLENILLEDDNCNIKIADFGLSNLYQKDKFLQTFCGSPLYASPEIVNGRPYRGPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YEFLETLGKGTYGKVKKARES-SGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Сарв
                                                                                                                                                                                                                                                                           Suzuki A., Kusakai G.-I., Kishimoto A., Lu J., Ogura T., Lavin M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: Expressed at high levels in heart and brain, and at lower levels in skeletal muscle, kidney, ovary, placenta, lung and liver.
SIMILARITY: Belongs to the Ser/Thr protein kinase family.
new cDNA clones from brain which can :ro.";
                                                                                                                                                                                                                                                                                                                                                    "Identification of a novel protein kinase mediating Akt survival signaling to the ATM protein.";
J. Biol. Chem. 278:48-53(2003).
-!- FUNCTION: Involved in tolerance to glucose starvation.
Phosphorylates ATM.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- ENZYME REGULATION: Activated by PKB/AKT1 during glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
;
                                                                                                                                                                     CHARACTERIZATION, AND MUTAGENESIS OF SER-600.
MEDLINE=22393479; PubMed=12409306; DOI=10.1074/jbc.M206025200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Indels
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61 YISERRRISERETRHFFRQIVSAVHYCHKNGVVHRDLKLENILLDDNCNIKIADFGLSNL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IKSIRKDKIKDELDMVHIRREIEIMSSLAHPHIISIYEVFENKDKIVIIMEYASKGELYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 IKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIHEVFENSSKIVIVMEYASRGDLYD
"Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: III. The Complete Nucleotide Sequences of 500 Mouse KIAA-homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Kandomly Sampled from Size-fractionated Libraries.";

DNA Res. 10:167-180(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 YISERPRISERDARHFFRQIVSALHYCHQNGIVHRDLKLENILLDANGNIKIADFGLSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name-ebig3238; ORFNames=ENSANGG0000012297;
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probom; PD000001; Prot Kinase; 1.
SWART; SW00210; S_TKC; 1.
SWART; SW00219; TyrKC; 1.
PROSITE; PS50011; TYROTEIN KINASE DOW; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL, AAABO1008879; EAABO421.1; -.
GO, GO:0005524; F:ATP binding; IEA.
GO, GO:0005474; F:strotein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                Okazaki N., Kikuno R., Nagase T., Ohara O., Koga H.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AB182364; BAD23995.1; --
InterPro; IPR01109; Kinase like.
InterPro; IPR001719; Prot_Kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR002219; Ser thr pkinase.
InterPro; IPR004245; Tyr pkinase.
PF00069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.4%; Score 1025; DB 2; Length 575;
82.3%; Pred. No. 1.3e-72;
cive 23; Mismatches 17; Indels
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.4%;
Best Local Similarity 82.3%;
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 5:31-39(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
Saga Y., Hagase T., Ohara O., Koga H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    698 AA; 78007 MW; BA3956E6C31EAE0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.1%; Score 1128.5; DB 2; 82.3%; Pred. No. 1.1e-80; ive 24; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JTL-2004 (TrEMBLrel. 27, Created) 05-JTL-2004 (TrEMBLrel. 27, Last seq. 05-JUL-2004 (TrEMBLrel. 27, Last ann MKIAA0537 protein (Fragment).
                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98290545; PubMed=9628581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB011109; BAA25463.2; -
NON TER 1 1
SEQUENCE 698 AA; 78007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                            KIAA0537 protein (Fragment).
KIAA0537.
                                                                                                                                                                                                                                                                         02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||:||:|:||
ATIEDIANHWWVNW 345
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| ATIEDIANHWWVNW 308
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                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                 BAA25463;
02-Mar-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohara O.;
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                                            295
                                                                                                                                                                                                               BAA25463
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                                                                                                                                           RESULT 7

BAA25463

BAA25463

AC BAA2

BD 02-19

BD 02-19

BD 02-19

BD C1-19

BD C1-1
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FLYBASE;
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     MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
An M.H., Doyle C., Baxer E.G., Helt G., Nelson C.R., Gabor G.L.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burtis K.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A clock A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                     60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
                                                                                                                                                                                                                                                                                     120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
                                                                                                                                                                                                                                                                                                                                           164 CHRDLKLENILLDEHGNAKIADFGLSNVFDEQRLLATFCGSPLYASPEIVKGTPYQGPEV 223
                                                                                                                                                                                                                                                                                                                                                                               DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR 239
                                                                                                                                                                                                                                                                                                                                                                                             224 DCWSLGVLLYTLVYGAMPFDGANFKRLVKQISQGDYFEPKKPSRASPLIREMLTVCPSHR 283
                                                                                                                                                                                                                       1 YEFLETLGKGTYGKVKKA-RESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH 59
                                                                                                                                                                                                Gaps
          InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr_pkin_AS.
Pfam; PF00069; Pkinase; I.
Probom; PD000001; PROTEIN KINASE ATP; I.
PROSITE; PS00107; PROTEIN KINASE DOM; I.
PROSITE; PS00109; PROTEIN KINASE STY, I.
PROSITE; PS00109; PROTEIN KINASE STY, I.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                    DB 2; Length 383;
GO:0006468; P:protein amino acid phosphorylation; IEA
                                                                                                                                                                   61.4%; Score 824.5; DB 2; Length 61.3%; Pred. No. 6.1e-57; ive 44; Mismatches 53; Indels
                                                                                                                                           383 AA; 43133 MW; 294732D45CFC1023 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 ANIEQICNHWWWN 296
                                                                                                                                                                                 Best Local Similarity 61.33
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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05-JUL-2004 (TrEMBLrel.
CG11870-PD.
ORFNames=CG11870;
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Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
Jalali M., Kaluab F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Liaz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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Menton D.R., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
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Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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Williams S.M., Woodagef W., Zhong G., Zhao G., Zhan G., Zhao G., Zhao G., Zhan G., Zhao K., Weisenback J.C.,
The genome sequence of Drosophila melanogaster.";
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frige E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22426065; PubMed=12537568; Carlson J.W., Halpern A., Calniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Calniker S.E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutron G.G., Venter C. Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.; Pfnishing a whole-genome shotgun: release 3 of the Drosophila
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the Ser/Thr protein Kinase family.
EMBL; AE003686; AAS65135.1; -.
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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InterPro; IPR000719; Prot Kinase.
InterPro; IPR000719; Prot Kinase.
InterPro; IPR008290; Sar Lhr pkinase.
InterPro; IPR008271; Ser Lhr pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PP00069; Pkinase; I.
ProDom; PD000001; Prot kinase; I.
SMART; SM00220; STKC; I.
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310 ASIEQICSHWWVN 322
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           Query Match
Best Local Similarity 61.77
Matches 156; Conservative
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                                                                                                                                                       10 FDIIKKLGQGTYGKVQLGINKETGQEVAIKTIKKCKIEAEADLVRIRREVQIMSSVHHPN 129
                                                                                                                                                                                              IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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                                                                                                                                         1 YEFLETLGKGTYGKVKKA-RESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH
                                                                                                                                                                                                                                                                                                            DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR
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LI SUMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; BT010033; AAQ22502.1; -.

R PlyBase; PESD10031940; CG11870.

R G0; G0:0004674; F:ATP binding;

R G0; G0:0004674; F:protein serine/threonine kinase activity; IEA.

G0; G0:0004674; F:protein serine/threonine kinase activity; IEA.

G0; G0:000468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR000219; Prot kinase.

R InterPro; IPR0002209; Ser thr pkinase.

R InterPro; IPR000209; Ser thr pkinase.

R InterPro; IPR000209; Ser thr pkinase.

R RAMAR; SM0000001; Prot kinase; 1.

R SMART; SM00107; Prof Kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R ROSITE; PS00109; PROTEIN KINASE DG; 1.

R ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 1180 AA; 127684 MW; 2CD790A4F3D8C5OC CRC64;
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threomine-protein kinase; Transferase.
SEQUENCE 1180 AA; 127743 MW; A88A012664046EC6 CRC64;
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                                                                            61.3%; Score 822.5; DB 2; Length 1180; 61.7%; Pred. No. 3.3e-56; Indels 1; ive 44; Mismatches 52; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                Conservative
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                                                                                                   Similarity
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Celniker S.;
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REAL MEDILINE=20196006; PubMed=10731132;

RADELINE=20196006; Richards S., Ashburner M., Henderson S.N., RADELINE, Radell M.D., Zhang Q., Chen L.X.,

RADELINE, RADELE E.G., Helt G., Nelson C.R., Gabor G.L.,

RADELINE, RADELE B.G., Helt G., Nelson C.R., Gabor G.L.,

RADELINE, RADELOS P.V., Berman B.P., Bhandari D., Bolshakov S.,

RADELINE, R.W., Cawley S., Butler H., Cadieu E., Center A., Chandra I.,

RADELINE, R.M., Cawley S., Dahlke C., Davenport L.B., Duvies P.,

RADELINE, R.D., E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RADELINE, RODELIS, Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RADELINE, RODELIS, GORGEN R., Gelbart W.M., Glasser K.,

RADELINE, RADELIS, RADELI
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                                                                                                                                                                1 YEFLETLGKGTYGKVKKA-RESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH
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    Length 1180;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Last annotation update)
    DB 2;
61.3%; Score 822.5; DB 2
61.7%; Pred. No. 3.3e-56;
iive 44; Mismatches 52
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J. S. S. Jakes

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10 FDIIKKLGQGTYGKVQLGINKETGQEVAIKTIKKCKIEAEADLVRIRREVQIMSSVHHPN 129
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Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodsgr, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22426065; PubMed=12537568;
Celniker S. B., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M., "Finishing a Whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.",
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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SEQUENCE 1180 AA; 127743 MW; A88A012664046EC6 CRC64;
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Matches 156; Conservative
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RAMADILINESCIBSO186005; Pubmed=10731132;

RAMADILINESCIBSO186005; Pubmed=10731132;

RAMADILINESCIBSO186005; Pubmed=10731132;

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RAMADILINESCIBSO186005; Recherer S.E., Holt K.A., Enbang O., Chen L.X.,

RAMADICO16.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RAME SULTON G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RAME SILVEN M.M. Basu A.M. Baxendale J., Bayraktaroglu L., Basaley E.M.,

RAME BESSON K.Y. Bence P.V., Barcerdale J., Bayraktaroglu L., Basaley E.M.,

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RAME BUTLIS K.C., Busam D.A., Leuler H., Bruck J., Broketein P., Brottler P., Brottler P.,

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RAME BUTLIS K.C., Busam D.A., Leuler H., Dayan-Rocha S., Dunkov B.C.,

RAME Dodoon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RAME DOSOON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RAME C., Gabrielian A.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RAME A. Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A.,

RAME A. M. Harvey D., Heiman T.J., Well M.H., Ibegwam C.,

Jaskop D., Lei Y., Karpen G.H., Kez., Kennison J.A., Ketchum K.A.,

Jaskop P., Lei Y., Levitsky A.A., Li J., Li Z., Mortis J., Moshrefi A.,

Monto S.M., Moy M., Murphy B., Murphy L., Murshy D.M., Nelson D.L.,

RAME B.C., Siden-Kiamos I. Simpson M., Strong R., Such B.,

Reinert K., Remington K., Saunders R., Venter E., Wang A.H.,

Spier E., Spradling A.C., Staplecon M., Strong S., Yao Q.A., Ye J.,

RAMI S.M., Woodager, Worley K.C. Wu D., Yang S., Yao Q.A., Ye J.,

Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RAME S. Tector C., Thurner R., Venter E., Wang A.H.,

RAMI S.M., Woodager, Worley K.C. Wu D., Yang S., Yao Q.A., Ye J.,

RAME S.M., Woodager, Worley R.W., Nelson D.,

RAME S.M., Woodager, Worley R.W., Nelson D.,

RAME S.M., Woodager, Worley R.W., Strong S., Yao Q.A., 
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MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Patel D.J.M., Park S., Peiffer B.D., Richards S., Sodergren E.J.,
Weinskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Héxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                              PRT; 1427 AA.
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Drosophila melanogaster (Fruit fly)
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01-MAR_2003 (TrEMBLrel. 23,
01-MAR_2004 (TrEMBLrel. 26,
CG11870-PA (CG11870-pb).
                            310 ASIEQICSHWWVN 322
240 ATLEDVASHWWVN 252
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                            MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AE001686; AAF54517.3; -.
INFACT; Q9VH05; -.
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                                                                                                                                                                                                                   Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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hes 156; Conservative
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REMEMBER OF CELNINGE TO STATE THE R.A. GOCAYDE J.D.,
RA Adams M.D. Celnikers S.E., Holf R.A. Evans C.A., Gocayne J.D.,
RA Adams M.D. Celnikers S.E., Holf R.A. Hoskins R.A., Galle R.F.
RA CHORGER S.E., Richards S., Ashburner M. Henderson S.N.,
George R.A., Levis S.E., Richards S., Ashburner M. Henderson S.N.,
RA Mannatides P.G., Scherer S.E., Helf G., Champe M., Pfelifer B.D.,
RA Brandon R.C., Nogers Y.H., Blazel R.G., Champe M., Pfelifer B.D.,
RA Brandon R.C., Robers Y.H., Blazel R.G., Champe M., Pfelifer B.D.,
RA Brandon R.C., Robers Y.H., Blazel R.G., Champe M., Pfelifer B.D.,
RA Brandon R.C., Robers Y.H., Blazel R.G., Champe M., Pfelifer B.D.,
RA Ballew R.M., Baavandale J., Bayraktsroglu L., Beasley B.M.,
RA Ballew R.M., Baun A., Baxendale J., Brokstein P., Brottler P.,
RA Borkova D., Botcher M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodon K., Cawleilan A.E., Garry N.S., Gelbart W., Classer R.,
RA Glodon K., Gong F., Gorrell J.H., Gu Z., Gulbar W., Touck J.,
RA Harris N.J., Bruscon R.A., Howland T.J., Wei M.H., I begwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., I begwam C.,
RA Jalai M., Kalush F., Kalpen G.H., Ke Z., Kuni Bon. J.A., Kethingon J.A., Kethingon J.A., Kalush P.,
RA Jalai M., Kalush F., Rapen G.H., Ke Z., Kuni Bon. J.A., Lasko P., Lei Y., Leviteky A.A., Li J.J., Marvitz S., Wolpherson D.,
RA Murkel B.E., Kodirac C.D., Kraft C., Krattle J., Morpherson D.,
RA Murkel B.E., Kodirac C.D., Kraft C., Krattle J., Morphersi A.,
RA Belson D.K., Milbhina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith H.O.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith H.O.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith H.O.,
RA Sheng Z.H., Woodager, Worley K.C., Wu D., Yang S., Yang S., Yang C.,
RA Zheng X.H., Zhong F.N., Weinstock G.M., Weinsenbach J.,
RA Zheng X.H., Woodager, Worley S., Woodager, Worley S., Pan S.,
RA Zheng X.H., Woodager, Worley S.
                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Eudopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                      01-APR-2004 (TrEMBLrel. 27, Created)
01-APR-2004 (TrEMBLrel. 27, Last sequence update)
01-APR-2004 (TrEMBLrel. 27, Last annotation update)
0311870-PA.
                                                                                                                     1427 AA
                                                                                                                       PRT;
310 ASIEQICSHWWVN 322
                                                                                                                     PRELIMINARY;
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                                                                                                                     AAF54517
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MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Patel D.J.M., Patk S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutron G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
"Finishing a Whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.",
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[3] SEQUENCE FROM N.A.

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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                          Waterston R.
                          Wilson R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
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                                                                                                                                                                                                                                                                                                                   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milbburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                         "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003686; AAF54517.3; -.
FlyBase; FBgn0037804; CG11870.
SEQUENCE 1427 AA; 153444 MW; 530928D0A057B5C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein B0496.3.
                                                                                                                                                                                                                                                                                                                                                                                                                    a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                           systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
MEDLINE=22426069; PubMed=12537572;
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Best Local Similarity 61.7<sup>3</sup>
Matches 156, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2002)
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                                                                                                                                                             Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase;
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180 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR 239
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GO; GO:0004674; F:ATP binding; IEA.

GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.

R GO; GO:00046468; P:protein amino acid phosphorylation; IEA.

R INTERPRO; IPR0009030; Graw_Erecept.

R INTERPRO; IPR000109; Kinase like.

R INTERPRO; IPR000109; Frot kinase.

R INTERPRO; IPR000209; Ser_thr_pkinase.

R INTERPRO; IPR000209; Ser_thr_pkinase.

R REAM: PR0000001; Prot kinase; 1.

R SWART; SM00107; Prot kinase; 1.

R ROSITE; PS00107; PROTEIN KINASE ATP; 1.

R ROSITE; PS00107; PROTEIN KINASE DOW; 1.

R ROSITE; PS00108; PROTEIN KINASE DOW; 1.

R ROSITE; PS00108; PROTEIN KINASE; COM; 1.

R RP-binding; Hypothetical protein; Kinase;

GW ATP-binding; Hypothetical protein; Kinase;

GW Serine/threonine-protein kinase; Transferase.
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1566;
                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein Kinase family.
EMBL, 108749; AAL65772.1; -.
HSSP, P31751; 1GZK.
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Murray J., Le T.T.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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ilarity 61.7%; Pred. No. 2.3e-55;
Conservative 33; Mismatches 63;
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Job time : 75.4118 secs
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Matches 156; Conserv
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SEQUENCE FROM N.A.
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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 11:04:39; Search time 5813.23 Seconds (without alignments)
11866.113 Million cell updates/sec

Title: US-09-980-464-4_COPY_123_2015
Sequence: 1893
Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750
Minimum DB seq length: 0
Maximum Match 100*

Dost-processing: Minimum Match 100*
Listing first 45 summaries

Database: EST:*
1: 9D_est1:*
2: 9D_est2:*
3: 9D_est2:*
3: 9D_est2:*
5: 9D_est2:*
5: 9D_est2:*
6: 9D_est5:*
7: 9D_est5:*
8: 9D_est6:*
9: 9D_est6:*
9: 9D_est6:*
9: 9D_est6:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	AK004737	AK033672	AK034082	AY399041	AY399039	AY399040	CB248251	CO424322	CK781308	BG174288	BG694881	BF789245	CA319312	CN261003	BM927376	BQ062868	BF785290	CF726196	BQ060729	BQ059508	BI143493	BQ064231	BB625283	BI648260
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æ	Query Match	100.0	100.0	98.1	93.7	9.99	50.1	36.1	35.5	34.5	34.4	34.1	34.1	33.8	33.2	32.5	32.0	31.9	31.5	31.0	31.0	30.5	30.3	29.7	29.5
	Score	1893	1893	1857.4	1773	1261	948.4	683.6	672	652.4	651.6	646	645.8	640	627.6	614.8	605.8	603	296	586.4	586.4	578	574.4	562.8	558.8
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BH116351 BM909401 BM909401 BC912964 BC912964 BC28581 CK483217 BQ085613 BQ08	BQ065997 CD632908 BQ056490 BQ055919
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ALIGNMENTS

RESULT 1 AKO04737 LOCUS DEFINITION ACCESSION VEYBORDS SOURCE ORGANISM TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS AUTHO	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone-1200013B22 product:weakly similar to PROBABLE SERIE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1) [Homo sapiens], full insert sequence. AK004737.2 GI:26334437 HTC: CAP trapper. HTC: CAP trapper. Mus musculus (house mouse) 1044821. Rodentia; Sciurognathi; Muridae; Murinae; Mus. Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253 10349636 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sakaguchi, S., Ikagami, T., Carninci, P., Waramatch, M., Inoue, Y., Tanaka, T., Matauncto, R., Matauncto, H., Sakaguchi, S., Ikagami, T., Kashiwade, S., Inoue, K., Togawa, Y., Tanaka, T., Maramatch, M., Inoue, Y., Marama, M., Ohara, E., Watahiki, M., Yokazaki, Y., Muramateu, M., Inoue, Y., Tanaka, T., Maramatch, M., Mara
REFERENCE AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE JOURNAL REFERENCE	Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) S

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weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE
KIAA0537 (EC 2.7.1.-) [Homo sapiens] (SWISSPROT|060285,
evidence: FASIY, 56.8%ID, 98.6%length, match=1849)"
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SMADWLRSSR PLLENGAKVCSFFKQHVPGGGSTVPGLERQHBLKKSKERUDMAQNLQ
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REIEIMSSLNHPHIIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFF
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On Dec 10, 2002 this sequence version replaced gi:12836134.

Please visit our web site (http://genome.gsc.riken.jp/) for further
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/tissue VPE="lung"
/clone lib="REN full-length enriched mouse cDNA library"
/dev_sfage="adult"
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                        Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 561-573 (2002)
6 (bases 1 to 2899)
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FANTOM Consortium and the RIKEN Genome Exploration Research
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AK033672 3098 bp mRNA linear HTC 03-APR-2004 Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130215K18 product:weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-) [Homo sapiens], full insert sequence.

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                                                                                                                                                                                                                           /note="unnamed protein product; putative weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-) [Homo sapiens] (SWISSPROT|060285, evidence: FASTY, 56.8%ID, 98.6%length, match=1849)"
                                                                                                                                                               /tissue_type="cecum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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                                                              /mol_type="mRNA"
| etrain="C57BL/64"
| db_xref="FANTOM_DB:9130215K18"
| db_xref="taxon:10090"
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                  organism="Mus musculus"
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
1. .3098
                                                                                                                                clone="9130215K18"
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TAAYRQALGICSKLS"
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REIEIMSSLNHPHIIAIHEVGRSRLVTVFENSSKIVIVMEYASRGDLYDYISERPRLS
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GTCGSBLYARABEINNGKPYVGEVDSWSLGYLLYILHGHPPBGQHHTLUKQISN
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PSGDFGRASMADWLRRSSRPLLENGAKVCSFPKQHVPGGGSTVPGLERGHSLKKSRKE
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Wanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGAGTCGGTGGCCTTACTCCAGCGCCCGAGCCAGGCTCCCTCGGCCTCCGCCCTGGCC 60
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The FANTOM Consortium and the RIKEN Genome Exploration Research
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="9330154N24"
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98.7%; Pred. No. 0;
ive 0; Mismatches
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/db_xref="GI:26329673"
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/strain="C57BL/6J"
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                                                                     GAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCTCCTCCCATCCTGCA 1712
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2869 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male diencephalon cDNA, RIKEN FULL-length
enriched library, clone:9330154N24 product:weakly similar to
PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                  GAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCTCCTCCCATCCTGCA
                                                                                                                        GCCCGGCCCAGCCCCCTCAGGGCTGTGAGGACAGCATCCTGTCCTCCGAGTCC
                                                                                                                                                                                                                           TITGACCAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCACTGAGGGGCTGTGTGTCT
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC 1985
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Meth. Enzymol. 303, 19-44 (1999)
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Direct Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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                    Gaps
                    21;
                    Indels
    Pred. No. 2.1e-236;
0; Mismatches 722;
   60.0%;
 Best Local Similarity 60.0°
Matches 1116; Conservative
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                                                                                                     CCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCT 1606
                                                                                                                       CCCAGACAGCCTTGGAGCTCGCGGCCCCCACCTTCGGCTCCCTGGATGAACTCGCCC 1585
                                                                                                                                                                                 CACCTCGCCCCCTGGCCCGGCCGGCCGCCTCTGGGGCTGTGAGCGAGGACGACCATCC 1645
                                                                                                                                                                                                                          TGTCCTCCGAGTCCTTTGACCAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCCACTGA 1726
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1 (bases 1 to 1887)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wanoy, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
CACAGGCTTCAGGGCTCCTCCTCCACCGCAAGGGCATTCTCAAACTCAATGGCAAGTTCT
                                                                                                                                                              CCTCCCATCCTGCAGCCCGGCCCAGCCGCCTCAGGGGCTGTGAGGAGGACAGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                        ACTGCCAAGAGGTGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1._.>1887
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Location/Qualifiers
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Pan troglodytes
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/mol type="mrmRnA"
/strain="C57BL/6"
/db_xref="rexon:1000"
/clone="InMGE:57BL/6"
/fevs stage="embryol 12: 5 dpc"
/fevs stage="embryol 12: 5 dpc"
/foloe lib="NIH BMAP_ED0"
/clone lib="Organ: brain; Vector: pXr-Asc; Site_1: BCOR I;
Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. Pirst strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was size selected according to mRNA size fraction, ligated with BCOR I adaptor, disested with Not I; and then cloned directionally into pXr.Asc vector: The library tag sequence located between the Not I site and the polyh tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
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Pred. No. 2.8e-167;
0; Mismatches 5;
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/organism="Mus musculus"
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       GCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACCCCTGGCCTGGAGCGCCAGC 1114
                                                                                                                                                                                      AGAAAAAGTCCTCTACCTCGTCAGGGGAGGTACAGGAGGACCCTCAGGAACTCAGACCGG 1306
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NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                       CTGAGGATACCTCTTCTCGCCCTGGCAAGAGCAGCCCTTAAGCTTCCGAAAGGCATTCTCA
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Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Institute of Mental Health (NIMH)."
                                                                            Score 672; DB 7;
Pred. No. 3e-164;
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'... 0; Mismatches
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/mol type="memorations"
/db_xerfe="csono:10090"
/clone="IMAGE:3065389"
/tissue_type="whole eye"
/dev_stage="memorations"
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

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Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pXx-5.
                            1338
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                                                                                                                                                                                                                                 1399 TACTCCTCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGACGCCAGTGATGTTTTGTG 1458
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 672)
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                   CAGGAGGACCCTCAGAACTCAGACCGGTGCCTGATACTCCAGGGCAGCCTGTCCCTGCT
                                                     AGTGGGGACCCCGTGGAGCAGAAGTCTCCACAGGCTTCAGGGCTCCTCCTCCACCGCAAG
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/organism="Mus musculus"
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1534 AATGGCAAGTTCTCCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCTG
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BG174288.1 GI:12680991
EST.
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BG174288
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/clone="Invascontriboto"
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/dev stage="whole brain"
/dev stage="whole brain"
/dev stage="mbryo 13.5,14.5,16.5,17.5dpc"
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/clone lib="NIH BMAP contains and lib="NIH Size"
/clone lib="NIH BMAP contains"
/clone lib="NIH BMAP contains"
/clone located between the Not I site and the cloned
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/clone Brain Anatomy Project (BMAP): 'Gene Discovery in the
/clone Brain Anatomy Project (BMAP): 'Gene Discovery in the
/clone Brain Anatomy Project (BMAP): 'Gene Discovery in the
/clone Brain Anatomy Project (BMAP): 'Gene Discovery in the
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/clone Brain Anatomy Project (BMAP): 'Gene Discovery in the
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/clone Brain Anatomy Project (BMAP): 'Gene Discovery in the
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/clone Brain Anatomy Project (BMAP): 'Gene Discovery in the
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1054 GCCAAGGTGTGCAGCTTCTTCAAGCAGCACGTGCGGGAGGTGGAAGCACTGTACCTGGG
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                                                                                                                                                                                                                                                                                                                                   1. .655
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6"
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Best Local 8
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/organism="Mus musculus"
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/strain="FVBIN"
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/dev_stage="3 months, virgin"
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/note="Torgan: mammary; Vector: pCMV-SPORT6; Sal1;
/note="Torgan: mammary; Vector: pCMV-SPO
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602334589F1 NCI_CGAP_Mam1 Mus musculus CDNA clone IMAGE:4457398 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is Theases 1 to 805)

is National Institutes of Health, Mammalian Gene Collection (MGC)

Al Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

Email: cgapbs-ramail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLAM10254 row: b column: 23

High quality sequence stop: 704.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to, 805)
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                                               481 AATGGCAAGTTCTCCCGCACAGCCTTAGAAGGCACTAACCCCTAGCACCTTTGGCTCCCTG
                                                                                                                                                                                                    GACCAACTGGCCTCCTCCCATCCTGCAGCCCGGCCCAGCCGCCCCTCAGGGGCTGTGAGT
                                                                                                                                                                                                                                                         1654 GAGGACCATCCTGCTCCTCCGAGTCCTTTGACCAATTGGACTTGCCTGAACGTC 1708
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                                             /tissue_type="nituitary gland"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B (phage-resistant)"
/clone_libe="Soares NMBP2 pituitary"
/note="Organ: brain; Vector: pT7T3D-Pac; Site_1: Not1;
Site_2: EcoR1; lst strand cDNA was primed with a Not1
oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTCTCGACAGCGTGAATCTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTGGGAAC
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                                                                                                                                                                                                                                                                                                                              34.1%; Score 646; DB 4; Le
100.0%; Pred. No. 1.9e-157;
tive 0; Mismatches 0;
 /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:4317546"
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 646; Conservative
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NISC: 1v09h10.w1 Soares NMBP2 pituitary Mus musculus cDNA clone
IMAGE:4317546 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 646)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can }
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                     CTAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCTCTCCAACCTGTACCAAAA
                                                                  GGCAAGTTCCTCCAGACGTTCTGTGGGAGCCCTCTTACGCCTCGCCTGAGATAGTCAAC
                                                                                                                                   GGGAAGCCCTATGTGGGCCCAGAGGTGGACAGCTGGTCTCTGGGCGTTCTCCTGTACATC
                                                                                                                                                                                                        CTGGTGCATGCCATGCCCTTTGACGGGCAGGATCATAAAACACTGGTGAAGCAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: W. Bento Soares Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
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Mus musculus
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BG694881.1 GI:13954237
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Seq primer: pYX-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="INAGE:4223267"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP Kidl4"
/note="Corgan: Kidney; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Corgan: Kidney; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidiarectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 GGTGAACCCCACCGTCGGGCCACACTGGAGGATGTAGCCAGTCATTGGTGGTCGACTAGTG 71
                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases 1 to 948)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 CCCTCAGGAACTCAGACCGGTGCCTGATACTCCAGGGCAGCCTGTCCCTGCTGTTATCCCT
                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tisaue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Http://mage.llnl.gov
Plate: LLAM0811 row: g column: 12
High quality sequence stop: 651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                867 GGTGAACCCCACCCGTCGGGCCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:10090"
                                                                 musculus (house mouse)
                               BF789245.1 GI:12094281
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                                                                     Mus musculus
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              ACCESSION
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AUTHORS
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/sine_1: The library was constructed according
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-866,
1996. Denatured RNA was size fractionated on a 1% agarose
gel: First strand cDNA synthesis was primed with oilso-dT
prime containing a Not I site Doble strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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Mus musculus (house mouse)

ENkaryord; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ENkaryord; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

ENkaryord; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Enkaryord; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Engass 1 to 795)

SS NIH-MGC http://mgc.nci.nih.gov/.

Inpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA bibrary Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra a:

Mustap.//mage.libray.ph.m.A.G.E. Consortium/Libra a:
                                                                                                                                                                  TCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGACGCCAGTGATGTGTTTGTGAGTGGGGA 1466
                                                                                                                                                                                                                                                                                                                                                                  1526
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UI-M-FW0-cbz-i-16-0-UI.rl NIH BMAP_FW0 Mus musculus cDNA clone
IMAGESEG16569 5', mRNA sequence.
1347 GCTCCCAAGGAAAGGCATCCTTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCCTC 1406
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CA319312.1 GI:24537436
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Query Match Best Local S: Matches 685

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derived_from H1, H7 and H9 cells"
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from embryoid body outgrowths derived from hES cell lines
H1 (p22), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, 1
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 782 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                 Score 627.6; DB 7;
Pred. No. 1.3e-152;
0; Mismatches 89;
                                                                                                                                                       /organism="Homo sapiens"
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Best Local Similarity 88.5%;
Matches 692; Conservative C
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                                                                                                        ATGGAGTCGGTGGCCTTACTCCCAGCGCCCAGGCTCCCTCGGCCTCCGCCTCGCCTTGGCC 140
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 782)

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Transcriptome characterization elucidates signaling networks that control human Es cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                         AAGCAGGCGGTGAAGCGGCACCATCACAAACAAACCTGCGGCACCGCTACGAGTTCCTG
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                                          Gaps
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                                          25;
     Length 795;
                                          Indels
   Score 640; DB 6; I
Pred. No. 7.3e-156;
); Mismatches 0;
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ilarity 96.5%;
Conservative
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REFERENCE AUTHORS JOURNAL

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/lab_host="lymptoms, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH1MGC_99"
/clone_lib="NH1MGC_91"
/note="Organ: llymptoms, vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/KhoI sites using the following 5' adaptor:
GGCACGAC(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
Library."
                                                                                                                                                                                                                                                                                                                   1069 bp mRNA linear EST 12-MAR-2002
-6704953 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5796791
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721 GAACCCCACCCGGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGTCAACTGGGG 780
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTCCGCCCTGGCCTCGGAGAGCGCCCGGCCGCTGGCGGACGGGCTCATCAAGTCGCCTA
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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/clone="IMAGE:5796791"
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Best Local Similarity 84.9%;
Matches 721; Conservative
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AUTHORS
TITLE
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APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: Martin, Unja
APPLICANT: Martin, Unja
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REPRENCE: 2923-A
CURRENT APPLICATION NUMBER: US/10/355,975
CURRENT FILING DATE: 2003-01-30
PRIOR PILING DATE: 2003-01-30
PRIOR PILING DATE: 2000-05-26
NUMBER: OF SEQ ID NOS: 36
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 4
US-10-302-172-215
US-10-342-172-215
US-10-343-514-13
US-10-322-281-21
US-10-363-829-151
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US-10-343-514-91
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US-10-343-514-93
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US-10-342-388-1541
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US-10-723-860-6703
US-10-723-860-6703
US-10-343-514-37
US-10-343-514-34
US-10-343-514-10
US-10-343-514-14
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US-10-343-514-14
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t; Pred. No. 0;
0; Mismatches
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Best Local Similarity 100.
Matches 1893; Conservative
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; ORGANISM: Mus musculus
US-10-355-975-4
                                                         56.0
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Sequence 1, Appli
Sequence 3, Appli
Sequence 45, Appl
Sequence 1, Appli
Sequence 13, Appli
                                                                                                                    January 24, 2005, 20:17:54; Search time 989.334 Seconds (without alignments) 10994.228 Million cell updates/sec
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Sequence 87, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Appl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                1 atggagtcggtggccttact......gaatctgctcaaagctcagc 1893
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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PUBLICATION NO. US20040132025A1
GENERAL INFORMATION:
APPLICANT: BRUCKER, Daniel J.
APPLICANT: BRUCKER, Daniel J.
APPLICANT: BRUCKER, Daniel J.
APPLICANT: LEFEBVRE, Diana L.
TILLE OF INVENTION: AMPRERELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REPERENCE: DPA-DRUCZ/PCT
CURRENT APPLICATION NUMBER: US/10/343,514
CURRENT APPLICATION NUMBER: US/01-01109
PRIOR FILING DATE: 2003-01-31
PRIOR PELING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2010-03-12
PRIOR APPLICATION NUMBER: US 60/224,613
PRIOR PRIOR APPLICATION NUMBER: C2 2,340,780
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 109
SOFTWARE PATENTIN VERSION 3.0
SEQ ID NO 27
LENGTH: 2026
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Pred. No. 0;
0; Mismatches 121; Indels
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Best Local Similarity 93.4%;
Matches 1769; Conservative
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; ORGANISM: RAT
US-10-343-514-27
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	September 1, Application US/10343514	421 CTGTATGATTACATCAGTGAGCGGCCACGGCTGAGTGAGCGGGACGCCAGGCATTTCTTC

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                                       CCAGGCATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACTGCCACCAGAACGGGATCG
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Patent No. US20020077312A1
GENERAL INFORMATION:
THIS OF INVENTION:
TITLE OF INVENTION: 3700, A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR
FILE REPERENCE: 10147-5001
CURRENT APPLICATION NUMBER: US/09/963,159
CURRENT FILING DATE: 2001-09-25
PRIOR PELING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 0;
0; Mismatches
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 10/217,168
PRIOR FILING DATE: 2002-08-12
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 119
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 1884
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APPLICANT: Hunter, John J.
APPLICANT: Hunter, John J.
APPLICANT: Hunter, John J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Curris, Rory A.J.
APPLICANT: Grait, Rery A.J.
APPLICANT: Galvin, Katherine M.
APPLICANT: Galvin, Katherine M.
APPLICANT: Hillamon, Mark J.
APPLICANT: APIGNAT: ABJOARSANAM
APPLICANT: Hillamon, Mark J.
APPLICANT: AND USES THEREFOR
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: AND USES THEREFOR
FRIOR APPLICATION NUMBER: US 100/218, 3543
FRIOR FILING DATE: 2002-10-22
FRIOR PELLING DATE: 2001-11-15
FRIOR FILING DATE: 2001-11-1
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Publication No. US20040058355A1
GENERAL INFORMATION:
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•	FALOR FILING DATE: 2000-09-21 NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin Ver. 2.1	R H	FEATURE: NAME/KEY: LOCATION: NAME/KEY:	; LOCATION: (3270) ; NAME/KEY: ungure ; LOCATION: (3272) US-09-963-159-1	Query Match 71.9%; Score 1360.2; DB 9; Length 3353; Best Local Similarity 84.2%; Pred. No. 0; Matches 1565; Conservative 0; Mismatches 273; Indels 21; Gaps 2;	QY 47 CCTCCGCCCTGGCCTCGGAGAGCGCCCGGCGGCGGAACGGGCTCATCAAGTCGCCTA 106 DD 191 CCACTCCTCGGCCGCAGAGCTGGCCGGCGCTGGAGGGCTGATCAAGTCGCCCA 250	QY 107 AACCTCTGATGAAGAAGAGAGAGACACCATCACAAACACAACCTGGGCACC 166 DD 251 AGCCCCTAATGAAGAAGAGAGGGGGTGAAGCAGCACCACACAAGCACAACCTGCGGCACC 310	Qy 167 GCTACGAGTTCCTGGAGACGCTGGGCACCTACGGGAAGGTGAAGAGGCACGAG 226 Db 311 GCTACGAGTTCCTGGAGACCCTGGGCAAGGCACCTACGGGAAGGTGAAGAAGGCGCGGG 370	Qy 227 AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGC 286 Db 371 AGAGCTCGGGCGCTGGTGGCCATCAAGTCAATCCGGAAGGACAAAATCAAAGTGAGC 430	Oy 287 AGGATCTGCTGCACATACGGAGGAGTTGAGATCATGTCTTCACTCAACCACCCCCACA 346	QY 347 TCATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATGTCATGAGTATG 406	QY 407 CCAGCGAGGGATCTGTATGATTACATCAGTGAGGGCCACGGCTGAGTGAG	Qy 467 CCAGGCATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACCACAGAACGGGATCG 526	Qy 527 TTCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG 586	QY 587 CTGACTTTGGCCTCTCCAACCTGTACCACAAGGCAAGTTCCTCCAGACGTTCTGTGGGA 646 Db 731 CTGACTTCGGCCTCTCCAACCTCACGATCAAGGCAAGTTCCTGCAGACATCTGTGGGA 790	QY 647 GCCCTCTGAGGCTGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAGAGGTGG 706 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 707 ACAGCTGGTCTCTGGGCGTTCTCCTGTACATCCTGGTGCACCATGCCATTGACG 766
	Oy 1007 TGGCGGACTGGTTACGTCCTCCTGGCCCCCTCCTGGAGAATGGAGCCAAGGTGTGCA 1066 Db 995 TGGCTGGACTCCTGGCGTTCCTCCCGCCCCTCCTGGAGAATGGGGCCAAGGTGTGCA 1054	Oy 1067 GCTTCTTCAAGGAGCACGTGCCGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGGCAAC 1126 Db 1055 GCTTCTTCAAGCAGCAACACCACCCCTGGCGCAAGCACCCCTGGCCTGGAGCCCCAGC 1114	OY 1127 ATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATCTGCAAGGTGACCCGG 1186	OY 1187 CTGAGGATACCTCTTCTCGCCCTGGCAGAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCA 1246	Oy 1247 AGAAAAGTCCTCTACCTCGGGGGGGGGGGCGCCCTCAGGAACTCAGACCGG 1306	OY 1307 TGCCTGATACTCCAGGGCAGCCTGTCCTGCTGTATCCCTGCTCCCAAGGAAGG	OY 1367 TTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCCTCTCCAAGCCCAGCGAGTCTG 1426	Qy 1427 GGGAACTCTTAGACGCCAGTGATGTTTGTGAGTGGGGACCCCGTGGAGAGTCTC 1486	OY 1487 CACAGGCTTCAGGGCTCCTCCTCCACGCAAGGCATTCTCAAACTCAATGGCAAGTTCT 1546 DD 1466 CGCAAGCTTCAGGGCTCCTCCTCCATCGCAAAGGCATCCTCAAATGGCAAGTTCT 1525	Oy 1547 CCCGGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCTACTGGCT 1606 Db 1526 CCCAGACAGCCTTAGAGCTCGGGGCCCCCACCACCACCTTCGGCTCCTGGATGAACTCGCCC 1585	QY 1607 CCTCCCATCCTGCAGCCCAGCCCCTCAGGGGCTGTGAGTAGGACAGCATCC 1666 DD 1586 CACCTCGCCCCTGGCCCGGCCCAGCCGACCCTCAGGGGCTGTGAGGGACAGCATCC 1645	Oy 1667 TGTCCTCCGAGTCCTTTGACCAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCACTGA 1726 DD 1646 TGTCCTCTGAGTCCTTTGACCAGCTGGACTTGCCTGAACGGTCCCCAGAGCCCCCACTGC 1705	OY 1727 GGGGCTGTGTGTGTGACAACCTGAGGGGGCCTTGAGCAGCCTCCCTC	Qy 1781GTCTGAAGCGATGGGAAGCAATCCTTGGGGGATAGCTGCTTTTCTCTGACAG 1834 Db 1766 GAAGCTGCCTGAGGGGCAGGATCCTTTGGGGACAGCTGCTTTTCCTGACAG 1825	Qy 1835 ACTGCCAAGAGGTGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC 1893 Db 1826 ACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCAAGCTCACC 1884		sequence 1, Application US/09963159 Patent No. US20020077312A1 GENERAL INFORMATION:

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                                1835 ACTGCCAAGAGGTGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC 1893
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                                                                                                    851 ACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGCATGCCCTTTGATG 910
                                                                                                                                                                                         AGCCGTCCGATGCCTGTGGCCTGATCCGGTGGCTGTTAATGGTGAACCCCCACCCGTCGGG 886
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AGCAACCTCAAGCTGCCAAAGGGCATTCTCA 1390

1331 CTGATGACACTGCCCATCGCCCTGGCAAGA 1247 AGAAAAGTCCTCTACCTCGTCAGGGGGGGGGG 1307 TGCCTGGTACTCCAGGCCTGTCCTG 1367 TTAGGAAGCTGTCCAGGCCTGCTGCT 1451 TCCCTGCGAGCCCAGGCCTGCTGCT 1502 TCAGAAAGTCTCTCAGGCCAGGCTTCTGCT 1457 TTAGGAAGTCTCTCAGGCCAGGCTTCTGCT 1457 TTAGGAAGTCTTTGAGCCTTGCTTGTT 1457 GGGAACTCTTAGACGCAGGCAGTTTGCTT 1457 GGGAACTCTTAGACGCAGCAGTTTGCTT 1457 GGGAACTCTTAGAGGCTCTCCTCCTCCCCCA 1487 CACAGGCTTCTAGAGGCTCTTCGCTGCT 1502 CCCAGACAGCCCTTCCTCCTCCTCCCCCAC 1547 CCCGCACAGCCTTCAGAGGCACTTCCCCCCAC 1547 CCCGCACAGCCTTTAGAGCTCCCCCCCCAC 1547 CCCGCACAGCCTTAGAGCCTCCCCCCCCCCCAC 1547 CCCGCACAGCCTTTAGAGCCTCCCCCCCCCCCCCCCACCCCCCCC	RESULT 10 US-10-311-034-38 Sequence 38, Application US/10311034 Publication No. US20040023242A1 GENERAL INFORMATION: APPLICANT: INCYTE GENOMICS, INC. APPLICANT: BANDWAN, Olga APPLICANT: BANDWAN, Olga APPLICANT: BANDWAN, Olga APPLICANT: BUROWSKY, Mark L. APPLICANT: BUROWSKY, Mark L. APPLICANT: GANDHI, Ameena R. APPLICANT: GREENWALD, Sara R. APPLICANT: GREENWALD, Sara R. APPLICANT: RARKORAR, Jayalaxmi APPLICANT: REBRINGR, Liam APPLICANT: BURFORD, Neil APPLICANT: BURFORD, Meil APPLICANT: BURFORD, Meil APPLICANT: BURFORD, Meil APPLICANT: MGUYSN, Danniel B. APPLICANT: MGUYSN, Danniel B. APPLICANT: HE, Ann
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	ACCGAGAGCCACCCAAGCCGTCCGATGCCTGTGGCCTGATCCGGTGGTTAATGGTGA ACCGAGAGCCACCACACTCCGATGCCTGTGGCCTGATCCGGTGGTTGATGGTGA ACCCCACCCGTCGGGCCACACTGGAGGATGTAGCCTGTTGGTGGGTTTGGTGGGGTTTGTTGGTGGGCTCAACTGGTGGGTTTAATGGTGAGGGTTTGTTGGTGGGGTTAATGGTGG	92 TIGGCCGGCCTCCATGGCGACTGGTTACGTCGCTCCTCGCGCCCCTCCTGGAGATG	n - n - n	1232 CGAAAGGCATTCTCAAGAAAAGTCCTCTCACCTCGTCAGGGGAGGTACAGGAGGACCCTC 1291	22 CARGEMAGGGATTCTCARGRAGIC COCCAGGGAGTCTGGTTTGTTACTCTCTCTCTCTCTCTCTCT	### ### ##############################
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### APPLICANT: THORNTON, Michael ### APPLICANT: HAFALIA, April ### APPLICANT: HAFALIA, April ### APPLICANT: GURURAJAN, Rajagopal ### APPLICANT: GURURAJAN, Rajagopal ### APPLICANT: GURURAJAN, Raiagopal ### APPLICANT: KHAH, Farrah A ### APPLICANT: RECIPON, Shirley A. ### APPLICANT: RECIPON, Shirley A. ### APPLICANT: RELIPOT, Vanifer L. ### APPLICANT: DING, Li ### APPLICANT: GRETHER, Megan ### APPLICANT: GLIOUT, Vicki S. ### APPLICANT: HANGAVELU, Kavitha ### APPLICANT: BATRA, Sajeev ### APPLICANT: ISON, Craig H. ### APPLICANT: ISON, Craig H. ### APPLICANT: HANGAVELU, KAVITHA ### APPLICANT: HOWAN KINASES	FILE REFERENCE: PI-0125 PCT CURRENT APPLICATION WUBBER: US/10/311,034 CURRENT APPLICATION WUBBER: 08/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372; FRIOR APPLICATION WUBBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372; 60/228,056 FRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-05; NUMBER: PERL PROGRAM SOFTWARE: PERL PROGRAM SEQ ID NO 38 LENGTH: 3360 TWE: DNA	Homo sapiens misc feature ORMATION: Incyte ID No. US20040023242A1 4841542CB1 -38 71.7%; Score 1357.6; DB 16; Length 3360; Similarity 83.7%; Pred. No. 0;	CCTCGGCCTCCGCCTGGCCTCGGAGGCCCCCGCCCTGGCGGAGGGC 91		Oy 272 AAATCAAAGATGAGGATCTGCTGCACATACGAGGGAGGATGAGATCATGTCTTCAC 331 Db 338 AAATCAAAGATGTGATGCACATACGAGGAGATTGAGATGATCATGTCATCGC 397 Qy 332 TCAACCCCCCACATCATTGCCATCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGA 391 Db 398 TCAACCACCCTCACATCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTGA 457	Qy 392 TTGTCATGGAGTATGCCAGCGAGGCGATCTGTATGATTACATCAGTGAGGGCCACGGC 451 Db 458 TCGTCATGGAGTATGCCAGCGGAGCGACCTTATGACTACAGCGAGCG

582 CTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCCATCGGAACAGGGTTG 641 527 TTCACCGAGATCTCAGAAACATCCTTCTAGATGCCATCGGAACAGGTTG 641 642 TCCACCGAGATCTCAGAACATCCTTCTAGATGCCAATGGAAACATCAGATTG 586 642 TCCACCGAGATCTCAACCTGGAACATCCTCTTGGATGCCAATGGGAATATCAAGATTG 701 587 CTGACTTTGGCTCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGAGATTG 701 702 CTGACTTCGGCTTCCAACCTGTACCACAAAGGCAAGTTCTTCTGGGA 616 704 CTGACTTCGGCTTCCAACTTAACGGGAAGTTCTTCTGTGGA 761 647 GCCCTCTCTAGGCTTCCCAACTTAACGGGAAGGTGCTTTTTTTT	762 GCCCCTCTATGCCTCGCCGAGATTGTCATAGGAGGCCCTACACAGGCCCTAGGGGGGGG	882 GGCATGACCATAAGATCCTGATGAAACGATCAGCAAGGGGGCCTCCTGGGGGGCCACCTA 941	dadadeadadetredeatodogradoeeaceerogoadadeareerogoadareerogoadeereerogoadatadeareerogoadadeareero	GCTTCTTCAAGCAGCACGAGGAGGAGGACACTGTACCTGGGCTGGAGCGCAAC [CTGAGGATACCTCTTCTCGCCCTGGCAAGAGCGACTTAAGCTTCCGAAAGGCATTCTCA [TGCCTGATACTCCAGGGCAGCCTGCTGCTGTATCCCTGCTCCCAAGGAAAGGCATCC	1427 GGGAACTCTTAGACGCCAGTGATTGTTTGTGAGGGACCCCGTGGAGGAGATCTC 1486 1533 GGGACTCTTGGACGCAGGGGTTTTGTGAGTGGGGACCCCGTGGAGGAGAGTCTC 1486 15497 CACAGGCTCTTGGAGGCTCTCTCCACCGCAAGGGGATTCTCTAACTCCAAGGAGAGCTC 1592 1497 CACAGGCTTCAGGGCTCTCTCACCCCAAGGCATTCTCAAACTCAATGGCAAGTTCT 1546 1593 CGCAAGCTTCAGGGCTGCTCCTCCATCGCAAGGCATCTCTAGGTTCT 1652
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1652 GTGAGGACAGCATCCTGCCGAGTCCTTTGACCAATTGGACTTGCCTGAACGTCTTC		RESULT 11 US-10-322-281-25 ; Sequence 25, Application US/10322281 ; Sequence 25, Application US/10322281 ; Publication No. US20040126762A1 ; GENERAL INFORMATION: ; APPLICANT: David W. Morris ; APPLICANT: Marc S. Malandro ; TILLE OF INVENTION: Novel Compositions and Methods in Cancer ; FILE REFERENCE: 229452001000 ; CURRENT FILING DAFE: 2002-12-17 ; UNRENT FILING DAFE: 2002-12-17 ; NUMBER OF SEO ID NOS: 86	SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 25 ; LENGTH: 3404 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-322-281-25	Query Match 71.7%; Score 1357; DB 17; Length 3404; Best Local Similarity 84.1%; Pred. No. 0; No. 0;			QY 347 TCATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATG 406 Db 462 TCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTGATCGTCATGGAGTATG 521 QY 407 CCAGCCGAGGCGATCTGTATGATTACATCAGTGAGCGGCCACGGCTGACTGA

407 CCAGCCGAGGCGATCTGTATGATTACATCAGTGAGCGGCCACGGCTGAGTGAG	823 GCCCCTCTATGCCTCGCCAGAGATTGTCATTGTCATTGTCTTTGTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGT	1067 GCTTCTTCAAGCAGCACCGGGAGCTGGAAGCACTGTACCTGGGCTGGAGCGGCAAC 1243 GCTTCTTCAAGCAGCACCACCTGGTGGGAAGCACCACCCTGGCCTGGAGCGCCCAGC 1243 GCTTCTTCAAGCAGCACCTGGTGGGGAAGCACCCCCTGGCCTGGAGCGCCCAGC 1127 ATCTCTCTAAGAAGTCCCGCAAGGAGAATCACTGCCAGCTCTCTCCAAGTGACACGG 1130 ATTCGCTCAAGAAGTCCCGCAAGGAGAATCACTGCCCAGTCTCTCCAAGTGACACGG 1136 ATTCGCTCAAGAAGTCCCCCAGCAAGAGAATCACCGG 1136 ATTCGCTCAAGAAGTCCCCTGGCAAGAGAACTCCCAGAAGAGCCATTCTCA
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227 AGAGCTCGGGGCCGTCTGGTGCCCATCAAGTCAACAGAAAACCAAAATCAAAGTCGGGCGGG	1160 GCTTCTTCAGGGGGGGGGGGGGGGGGGCCCCCCCTGGCCTGGGCGGGGCGGGGGG
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1127 ATTCTCTTAAGAAGTCCCGAAAGGAGAATGACTCAAAATCTGCAAGGTGACCCGG 1186
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CCACTCCCTCGGCCGCAGAGCTAGCCCGGCCGCTGGAGGGCTGATCAAGTCGCCCA
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                                    227 AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGC
                                                                                                                                                                     AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACA
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                          AACCTCTGATGAAGAAGCAGGCGGTGAAGCGGCACCATCACAAAACACAACCTGCGGCACC
                                                                         GCTACGAGTTCCTGGAGACGCTGGGCAAGGCACCTACGGGAAGGTGAAGAAGACGCACGAG
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                                                                CACAGGCTTCAGGGCTCCTCCTCCTCCCAGGGCATTCTCAAACTCCAATGGCAAGTTCT
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                     GGGAGCTCTTGGACGCAGGCGTGTTTGTGAGTGGGGATCCCAAGGAGCAGAAGCCTC
       TGCCTGATACTCCAGGGCAGCCTGTCCCTGTATCCCTGCTCCCAAGGAAAGGCATCC
                                                     TTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTG
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APPLICANT: BODARY, SARAH C.
APPLICANT: BODARY, SARAH C.
APPLICANT: BISDELL, HUNTE
APPLICANT: BRISDELL, HUNTE
APPLICANT: JACKWAN, JANET
APPLICANT: WILLIAMR, P. MICKEY
APPLICANT: WILLIAMR, P. MICKEY
APPLICANT: WILLIAMR, P. MICKEY
APPLICANT: WILLIAMR, P. MICKEY
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WU, THOMAS D.
ITILE OF INVENTION: Related Diseases
FILE REFERENCE: P1948R1-US
CURRENT APPLICATION NUMBER: US/10/370,7158
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 639, Application US/10370715B Publication No. US20040258678A1 GENERAL INFORMATION:
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 94.0%;
Matches 1114; Conservative C
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: RAT-:
US-10-343-514-13
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Publication No. US20040132025A1

GENERAL INFORMATION:

APPLICANT: DRORMATION:

APPLICANT: BRUCKER, Daniel J.

APPLICANT: BRUCKER, Daniel J.

APPLICANT: LEFEBURE, Daniel J.

APPLICANT: LEFEBURE, Daniel J.

TILE OF INVENTION: AMPR-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REFERENCE: DPA-DRUCZ/PCT

CURRENT APPLICATION NUMBER: US/10/343,514

CURRENT FILING DATE: 2003-01-31

PRIOR PRILING DATE: 2000-08-02

PRIOR PLICATION NUMBER: US 60/222,650

PRIOR PLICATION NUMBER: US 60/224,613

PRIOR PLICATION NUMBER: US 60/224,613

PRIOR PLICATION NUMBER: CA 2,340,780

PRIOR PLILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 109

SEQ ID NO 13
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                                    AGAAAAAGTCCTCTACCTCGTCAGGGGAGGTACAGGAGGACCCTCAGGAACTCAGACCGG 1306
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| 030 TCGCGCCCTCCTGGAGAATGGAGCCAAGGTGTCTTCTCAAGCAGCACGTGCCG 1089 | 1030 TCGCGCCCTCCTGGAGAATGGAGCCAAGGTGTGCTTCTTCAAGCAGCACTGTGCCG 1020 | 1090 GGAGGTGGAACCTGTACCTGGAACGCAACTTCTTCTTCAAGCAGCTGTGCCG 1020 | 1090 GGAGGTGGAACCTGTACCTGGAACGCGCAACATTCTCTTTAAGAAGTCCCGAAAG 1149 | 1021 GGAGGTGGAACCGGGTGGAGCGCGCAACATTCTCTTAAGAAGTCCCGAAAG 1140 | 1001 GAGATGACAGCGCAAAATCTGCAAGAGCGCCAAGATGCCCCAAGAACCCCGCAAG 1080 | 1150 GAGAATGACAGCACAAAATCTGCAAGAAAAAGTCCCCCATGAAGAAAAACTCCCCCCTTCCCCCCT 1140 | 1081 GAGAATGACATGCTTCGCAAAATCACCCAAGAAAAAG 1254 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 11111 | 11111 | 11111 | 11111 | 11111 |
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Search completed: January 25, 2005, 07:55:10 Job time : 996.334 secs

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Sequence 1257, Ap
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-355-9758-4
US-09-984-890-1
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138, Appli
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Patent No. 651419
GENERAL INFORMATION:
APPLICANT: Bird, Timothy A.
APPLICANT: Wirca, G. Duke
APPLICANT: Wartin, Unja
TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-A
CURRENT PILICATION NUMBER: US/09/579,664B
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 4
SEQ ID NO 4
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US-09-523-849-3

US-09-16-126-13

US-09-167-322-3

US-09-167-322-3

US-09-167-322-3

US-09-17-197-10

US-09-17-197-138

US-09-17-197-138

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US-09-12-771-1

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US-09-016-434-1454
US-09-590-740-5
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Best Local Similarity 100.0%;

Matches 1893; Conservative 0
TYPE: DNA
, ORGANISM: Mus musculus
US-09-579-6648-4
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GCTTCTTCAAGCAGCAGCAGGAGGAGGAGGAGCACTGTACCTGGGCTGGAGCGCAAC 1126
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| Patent No. 6492156
| ABREAL INFORMATION:
| TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
| TITLE OF INVENTION: THEREOF
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                                    ATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATCTGCAAGGTGACCCGG
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                       TGGCGGACTGGTTACGTCGTCCTCGCCCCCTCCTGGAGAATGGAGCCAAGGTGTGCA
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US-09-799-451-215
  TYPE: DNA
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Pred. No. 2.1e-47;
0; Mismatches 344; Indels
CURRENT APPLICATION NUMBER: US/09/984,890
CURRENT FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Best Local Similarity 54.9
Matches 422; Conservative
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ORGANISM: Homo sapiens
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US-09-984-890-1
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPREBUCE: CLOO01306D1V
CURRENT APPLICATION NUMBER: US/10/274,194
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Pred. No. 2.1e-47;
0; Mismatches 344;
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Local Similarity 54.9%;
nes 422; Conservative (
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ORGANISM: Homo sapiens
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Matches
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US-09-270-767-1257/c

US-10-274-194-1
; Sequence 1, Application US/10274194
; Patent No. 6706511
; PATENT NO GRANAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.

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Sequence 1. Application US/09930181

Sequence 1. Application US/09930181

Patent No. 6455292

GRNERAL INFORMATION:

APPLICANT: OriGene Technologies

TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas CURRENT PILINE DATE: 2001-08-16

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.0

SEQ ID NO. 1
                                                                                          442 CCGGCCAGGAGGTGGCTATCAAAACCATCAAGAGGTGCAAGATCGAGGCCGAGGCGGGATT 383 😁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 GAGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 TCGGTGCTGATGAAGGTGGAGCGGGAGATCGCGATCCTGAAGCTCATTGAGCACCCCAC 336
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                                                   233 CGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGGGGTC 292
                                                                                                                                  TGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACATCATTG 352
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Pred. No. 1e-42;
0; Mismatches 356;
            Mismatches 158;
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Best Local Similarity 53.5%;
Matches 413; Conservative
            Conservative
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; LOCATION: (106)..(2112)
US-09-930-181-1
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ORGANISM: Homo
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            Matches 284;
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US-09-930-181-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccesccaggagstesctatcaaaaccatcaagaastecaagatcgagsccgaggcggatt 383
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Sequence 1257, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION

APPLICANT: Homburger et al.

TITLE REPERENCE: FILE REFERENCE: FILE REFERENCE: FILE REPERENCE: FOR 17876-094

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 1257
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE PERERENCE: File Reference: 7326-094
CURRENT PILING DATE: 1999-03-17
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTI VET. 2.0
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; Sequence 16539, Application US/09270767
; Patent No. 6703491
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Patent No. 6258547

GENERAL INFORMATION:

APPLICANT: Beri, Rajindar K.

APPLICANT: Beri, Rajindar K.

APPLICANT: Porder, Robert A.

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/08/557,006C

CURRENT APPLICATION NUMBER: US/08/557,006C

CURRENT APPLICATION NUMBER: BCT/GB94/01093

PRIOR APPLICATION NUMBER: GB 9310489.1

PRIOR FILING DATE: 1993-06-21

PRIOR FILING DATE: 1993-06-21

PRIOR FILING DATE: 1993-06-31

PRIOR FILING DATE: 1993-06-31

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIN Ver. 2.1
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                                                                                   GAAGCAGGCGGTGAAGCGCCATCACAAACACAACCTGCGGCACCGCTACGAGTTCCT
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APPLICANT: Carling, David
APPLICANT: Porder, Robert A.
TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
FILE REFERENCE: NGAP/PHM37588/UST
CURRENT APPLICATION NUMBER: US/08/557,006C
CURRENT FILING DATE: 1996-00.06
PRIOR APPLICATION NUMBER: PCT/GB94/01093
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d. No. 1.3e-41;
Mismatches 381;
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                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: cDNA of rat;
COTHER INFORMATION: liver AMP protein kinase
US-08-557-006C-24
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                                                                                                                                                                                                                                Score 182.4; DB 3; Length 2761;
Pred. No. 1.3e-41;
0; Mismatches 381; Indels 6;
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     PRIOR FILING DATE: 1994-05-20
PRIOR APPLICATION NUMBER: GB 9310489.1
PRIOR FILING DATE: 1993-05-21
PRIOR FILING DATE: 1993-06-31
PRIOR FILING DATE: 1993-08-31
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
                                                                                                                                                                                                                                    tch 9.6%;
al Similarity 53.0%;
437; Conservative
                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Seguence
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US-08-557-006C-38

(S-08-557-006C-38, Application US/08557006C)

(Sequence 38, Application US/08557006C)

(BADELIA INNOWANION:

(APPLICANT: Beri, Rajindar K.)

(APPLICANT: Carling, David

(APPLICANT: Carling, David

(APPLICANT: Carling, David

(APPLICANT: Robert A.)

(TILE REFERENCE: NGAP/PHM37588/UST

(CURRENT APPLICATION NUMBER: US/08/557,006C

(CURRENT FILING DATE: 1996-03-06

(PRIOR APPLICATION NUMBER: EPT/GB94/01093

(PRIOR APPLICATION NUMBER: GB 9310489.1)

(PRIOR PILING DATE: 1994-05-20

(PRIOR PILING DATE: 1993-05-21

(PRIOR PILING DATE: 1993-06-31

(PRIOR PILING DATE: 1993-08-31

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Local Similarity 53.1%; Pred. No. 2.3e-41;
les 434; Conservative 0; Mismatches 378;
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1080 TGTGTGGAGTCTTTTTATACACTAGTCAGTGGCTCACTTCCCTTTGATGG 1139
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                                         288 GGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCACAT
                                                                                 660 AAGTCTACAAAAGCTCTTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATCCCAATAT
                                                                                                                      348 CATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATGC
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APPLICANT: Wang, Dunrui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743619e1 Nucleic P.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
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Zhou, Ping
Goodrich, Ryle
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Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
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Wang, Jian-Rui
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Asundi, Vinod
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                                                                                                                    GCTCTTTAAGAAGATCCGAGGGGGTGTGTTCTACATCCCGGAGTATCTCAACCGTTCTAT 722
                                                                                                                                                                                                 TGCCACTCTGCTGATGCACGTGCTGCACCCCTTGAAGCGAGCAACTATCAAAGA 782
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CGTTCTCCTGTACATCCTGGTGCATCGTGCCATCATTGATCGTGGGCAGGATCATAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: KINASE
                                                                                                                                                                                                                                                                            783 CATACGAGGGATGAATGGTTTAAACAGGATTTGCCCA 820
                                                                                                                                                                                                                                       900 TGTAGCCAGTCATTGGTGGGTCAACTGGGGGTTACACCA 937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
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Pred. No. 7.2e-41;
0; Mismatches 352
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09-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palace."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 5.3.
ATTONNEY AGENT INFORMATION:
NAME: CATUTHER, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 9-96
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2698 base pairs
                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08677298
Patent No. 5863729
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APPLICATION NUMBER: US
FILING DATE: 09-JUL-19
CLASSIFICATION: 536
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TITLE OF INVENTION: KIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, 1
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US-08-677-298-1
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Best Local Simi
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; NAME/KEY: CDS
; LOCATION: (482)..(2239)
US-09-930-181-3
                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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                                                                                                                           Length 2899
                                                                                                                           Score 176.4; DB 4; Length
Pred. No. 7e-40;
0; Mismatches 371; Indels
SOFTWARE: pt_FL_genes Version
SEQ ID NO 112
LENGTH: 2899
                                                                                                                             Query Match
Best Local Similarity 52.4%;
Matches 412; Conservative
                                                                           ; NAME/KEY: CDS
; LOCATION: (119)..(2899)
US-09-774-528-112
                                                  ORGANISM: Homo sapiens
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RESULT 14 US-09-930-181-3

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Sequence 3, Application US/09930181
Patent No. 6455292
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
FILE REPERENCE: 160 101 V1
CURRENT APPLICATION NUMBER: US/09/930,181
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
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Pred. No. 3.6e-39;
0; Mismatches 355; Indels
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Best Local Similarity 53.4%;
Matches 414; Conservative
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  1000 ACGCCCCCCCACGCTAGAGCACATTCAGAAACACATATGGTATATAGGGGGCAAGA 1055
                                                                              US-10-003-690-3

Sequence 3, Application US/10003690

Sequence 3, Application US/10003690

Patent No. 6787345

GENERAL INFORMATION:

APPLICANT: ROTY A.J. Curtis

TITLE OF INVENTION: 55053, A No. 6787345el Human Eukaryotic Kinase

TITLE OF INVENTION: and Uses Therefor

FILE REFERENCE: MNI-206

CURRENT APPLICATION NUMBER: US/10/003,690

CURRENT FILING DATE: 2001-11.15

PRIOR APPLICATION NUMBER: 60/248,893

PRIOR FILING DATE: 2000-11-15

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.1%; Score 173; DB 4; Length 2334; Best Local Similarity 52.7%; Pred. No. 5.8e-39; Matches 399; Conservative 0; Mismatches 355; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (1)...(2334)
US-10-003-690-3
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2334
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January 24, 2005, 05:56:58; Search time 875.636 Seconds (without alignments) 11348.500 Million cell updates/sec Run on:

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1 atggagtcggtggccttact......gaatctgctcaaagctcagc 1893 score: Sequence: Title: Perfect

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4134886 segs, 2624710521 residues Searched:

8269772 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseq 23Sep04:* Database

genesequ1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES	Description	AAC90433 Murine Ly	AAD31710	ADL14162 Novel hum	ABK14000 CDNA enco	ADL14160 Novel hur	AAD26459 Auman kin	AAK94280 Human ful	ADL30885 Full leng	ADJ96554 Human ca	ABZ11333 Auman pol	ADM43851 Novel hum	ABX71420 Abx71420 Human cel	ADF76964 Novel hun	ADF81952 Leukaemia	ADO20171 Ado20171 Human PRO	AAF44659 Novel pro	ADI29357 Human MAR	AAF75338 Human TGF	ABZ77163 Abz77163 Human pro	ABQ72599 Auman MDD	
U)	Ü	AACS	AAD3	ADI	ABK1	ADI	AAD2	AAK9	ADI	AD	ABZ1	ADV	ABX7	ADE	ADF	ADC	AAF4	ADI	AAF7	ABZ	ABQ7	
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de	Query Match	100.0	88.9	71.9	71.9	71.9	71.7	71.7	71.7	71.7	71.6	71.6	71.6	71.6	71.6	71.6	70.7	70.7	69.4	65.0	44.4	
	Score	1893	1683.4	1360.2	1360.2	1360.2	1357.6	1357	1357	1357	1355.4	1355.4	1355.4	1355.4	1355.4	1355.4	1338.8	1338.8	1314.2	1230	840.2	
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Aad14328 Human pro	Aad14327 Human pro	Ade38420 Human pro	Adn95767 Human BEC	Adj74808 Marker ge	Adl25352 Human ARK	Adq19733 Human sof	Adp43253 Human pro	Human		Aak93296 Human cDN	Aak91887 Human cDN	Ad129723 5' end of	Ad128314 5' end of	Abl21269 Drosophil	Aah13802 Human cDN	Aaf44655 Novel pro	Aal60326 Human 207	Adi29353 Mouse MAR	Aba05737 Murine ne	Aba05738 Murine ne	Abs64386 Human ser	Aad51409 Human mic	Adg91747 Human mic
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26.8	26.8	26.8	26.8	26.8	26.8			26.8						15.7	14.1	12.5	12.5	12.5	12.5	12.5		m.	12.3
506.4	506.4	506.4	506.4	506.4	506.4	506.4	506.4	506.4	356.8	348.8	348.8	348.8	348.8	296.8	267	236.6	236.6	236.6	236.6	236.6	233.6	233.6	233.6
22	23	24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

Murine; Lymph node Stromal cell kinase; MLSK-1; autoimmune disorder; wound healing; periodontal disease; inflammatory disease; tumour; infection; allergy; ss. Murine Lymph node Stromal cell kinase 1 coding sequence. Martin U, Anderson DM; ВР. AAC90433 standard; cDNA; 2902 26-MAY-2000; 2000WO-US014696. 99US-0136781P 19-MAR-2001 (first entry) (IMMV) IMMUNEX CORP. Virca GD, WO200073468-A1. 28-MAY-1999; Mus musculus. 07-DEC-2000. AAC90433; Bird TA, AAC90433

Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses.

WPI; 2001-061546/07. P-PSDB; AAB50056.

Claim 1; Page 86-87; 106pp; English.

The present sequence is the coding sequence for Murine Lymph node Stromal cell kinasa I (MLSK-1). The protein encoded by the present sequence is useful for treating a variety of disorders listed in the disclosure of the specification, including autoimmune disorders, allergic reactions, mayeloid or lymphoid cell deficiencies, wound healing and tissue repair and replacement, burns, incisions and ulcers, periodontal disease, inflammatory diseases, tumoures and bacterial, viral or fungal infection

XX SQ Se Query Beat Match	Sequence 2902 BP; 654 A; 794 C; 796 G; 658 T; 0 U; 0 Other; Query Match 100.0%; Score 1893; DB 4; Length 2902; Best Local Similarity 100.0%; Pred: No. 0; Matches 1893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1083 1021 1143	CTGCGTGAGGGTGGGCACCCTAGTGGTGACTTTGGCCGGGCCTCCATGGCGGACTGGTTA 1142 CGTCGCTCCTCGCGCCCCTCCTGGAGAATGGAGCCAAGGTGTGCACTTCTTCAAGCAG 1080	,
ò a	႘ႍႍ႘	Qy 1081 CACGTGCCGGGAGG 	CACGIGCCGGGAGGIGGAAGCACTGTACCTGGGCTGGAGCGGCAACATTCTCTTAAGAAG 1140 	
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& a		Oy 1201 TCTCGCCCTGGCAA	TCTCGCCCTGGCAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCAAGAAAAAAGTCCTT 1260 	
& g	GAGA CGCTGGGCAAGGCCACCTACGGGAAGGTGAAGAAGGCACGAGAGAGCTCGGGGCGT 	Oy 1261 ACCTGGTCAGGGGA 	ACCTCGTCAGGGAGGTACAGGAGGACCCTCAGGAACTCAGACCGGTGCCTGATACTCCA 1320 	
% q	TGGTGGCCATCAGTCCATCAGAAAGACAAATCAAAGATGAGCAGGATCTGGTGCAC	Oy 1321 GGGCAGCCTGTCCC	GGGCAGCCTGTCCTGTTATCCCTGCTCCCAAGAAAAGGCATCCTTAAGAAGTCTCGA 1380 	
<i>∂</i> 8		Oy 1381 CAGCGTGAATCTGG	CAGCGTGAATCTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGAC 1440 	,
% a	GAAGTOTTTGAGAATACCAGCAAGATTGTGATTGTCATGGAGTATGCCAGCCGAGCGAT 	Qy 1441 GCCAGTGATGTGTT	GCCAGTGATGTGTGAGGGGACCCCGTGGAGCAGAAGTCTCCACAGGCTTCAGGG 1500 	
, S		Oy 1501 CTCCTCCACCG	CTCCTCCACCGCAAGGGCATTCTCAAACTCAATGGCAAGTTCTCCCGCACAGCCTTA 1560 	
که م م	CGACAGATCGTGTCTGCCTGCACTACTGCCACCAGAACGGGATCGTTCACCGAGATCTC	Qy 1561 GAAGGCACTACCCC	GAAGGCACTACCCTAGCACTTTGGCTCCCTGGACCAACTGGCCTCCTCCCATCCTGCA 1620	£
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y dg	TCCAACTGTACCACAAAGGCAAGTTCTCCCAACGTTCTGTGGGAGCCTCTCTTACGCC	Qy 1681 TTTGACCAATTGGA 	TTTGACCAATTGGACTGCCTGAACGTCTTCCCGAAACCCCACTGAGGGGCTGTGTGTCT 1740 	
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8 %		Oy 1861 AGACAAGCCCTAGG 	agacaagccctaggaatctgctcaagctcagc 1893 	٠
ර සි	841 TGTGGCCTGATCCGGTGGTGTTAATGGTGAACCCCACCGGTGGGGCACCTGGAGGAT 900	RESULT 2 AAD31710 ID AAD31710 standard; cDNA;	; 2929 BP.	
6 Q	901 GTAGCCAGTCATTGGTGGGTCAACTGGGGTTACACCACCGGAGTCGGGGAACAGGAAGCC 960 	XX AC AAD31710; XX DT 18-JUN-2002 (first entry)	EY)	
À	961 CTGCGTGAGGGTGGGCACCCTAGTGGTGACTTTGGCCGGGCCTCCATGGCGGACTGGTTA 1020	XX DE Rat SNF1/AMPK-Related Kinase (SNARK) XX	inase (SNARK) cDNA.	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an AMPK (AMP-activated protein kinase) -related kinase, designated SNARK polypeptides and polynucleotides. SNARK (SNIF/AMP-activated protein kinase) is involved in stress response to glucose deprivation. The polynucleotides are useful for expressing SNARK protein in isolated form or as a protein conjugate. Activation of SNARK stimulates liver CPT-1 thus enhances lipid metabolism in liver cells and in other cell types such as heart and skeletal muscles, as well as increases GLUT-4 and glycogen in muscle. Activation of SNARK is predicted to have insulin-like effects that would enhance the disposal of glucose CC into muscle and reduce plasma glucose for the treatment of diabetes and some type of disorders of lipoprotein production leading to increased come type of disorders of lipoprotein production leading to increased levels of cholesterol or triglycenides. SNARK or its variants may be administered to a subject to treat or prevent a disease associated with decreased expression of SNARK, such as diabetes. SNARK antibodies are cused to modulate SNARK activity either in vivo for therapeutic purposes. SNARK antagonists may be administered to increase fuel production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucose uptake and increase levels of blood glucose in a patient g from hypoglycaemia. The present sequence is rat SNARK cDNA
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Rat; SNF1/AMPK-Related Kinase; SNARK; enzyme; stress response; diabetes; glucose deprivation; lipid metabolism; therapy; lipoprotein disorder; hyperglycaemic; drug screening; hypoglycaemia; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMPK (AMP-activated protein kinase)-related kinase, designated SNARK polypeptides and polynucleotides, useful for treating or preventing diabetes, or other disorders of lipoprotein production leading to increased levels of cholesterol.
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                                                                                                                                                               /product= "Rat SNARK
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                                                                                                         Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        Lefebvre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example, Fig 2; 94pp; English
                                                                                                                                                                                                                                                                                                           03-AUG-2000; 2000US-0222650P.
12-MAR-2001; 2001US-0274613P.
28-MAR-2001; 2001CA-02340783.
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Matches 1769; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAE19885.
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1261 ACCTCGTCAGGGGAGGTACAGGAGGACCCTCAGGAACTCAGACCGGTGCCTGATACTCCA 1320

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cell proliferation; cell differentiation; cell growth; cell division;
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                  human; gene; ss.
                                             Homo sapiens
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    Antiarchritic; antiarcheumatic; cardiovascular; varucide; analgesic; antiarcheumatic; cardiovascular; virucide; analgesic; antiapsoriatic; antiasthmatic; cardiovascular; virucide; analgesic; CNS; antipsoriatic; antithror; angiogenesis stimulator; cerebroprotective; wangiogenesis stimulator; cerebroprotective; cell proliferation disorder; cell differentiation disorder; platelet disorder; immune disorder; platelet disorder; immune disorder; metabolism disorder; immune disorder; metabolism disorder; immune disorder; metabolism disorder; viral disease; pain disorder; metabolic disorder; neurological disorder; viral disease; pain disorder; central nervous system disorder; erythroid disorder; metabolism; disorder; cancer; heart failure; whypertension; angina; osteoarthritis; rheumatoid arthritis; multiple sclerosis; Crohn's disease; psoriasis; asthma;
                                                               CAGCGTGAATCTGGTTACTACTCCTCTCCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGAC 1440
                                                                                                                  CAGCGTGAATCTGGTTACTACTCCTCTCCAGAGCCCAGTGAGTCTGGGGAACTCTTAGAC 1522
                                                                                                                                                                                                               1501 CTCCTCCTCCACGCAAGGGCATTCTCAAACTCAATGGCAAGTTCTCCCGCACAGCTTA 1560
                                                                                                                                                                                                                                 ---CGCCTCCATCGCAAGGCATCCTCAAACTCAATGGCAAGTTTTCCCGCACAGCCTTA 1639
                                                                                                                                                                                                                                                                     GAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCTCCTCCCATCCTGCA 1620
                                                                                                                                                                                                                                                                                               1640 GAAGGCACTGCCCCTAGCACCTTTGGCTCCCTAGACCAACTGGCCTCCCCTCATCCTACA 1699
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                                             GGGCAGCCTGTCCCTGCTGTATCCCTGCTCCCAAGGAAAGGCATCCTTAAGAAGTCTCGA 1380
                                                                                                                                                        GCCAGTGATGTGTTTGTGAGTGGGGACCCCGTGGAGCAGAAGTCTCCACAGGCTTCAGGG 1500
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                                                                                                                                                                        cytostatic; cardiant; hypotensive; antianginal; osteopathic;
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The invention describes an isolated 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (1) comprising any one of 40 nucleotide sequences (1). The nucleic acid molecules and polypeptides are useful for diagnosing and treating a subject having a disorder, or a subject at risk of developing a disorder, which is associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501,
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Chun M, Williamson MJ;
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Galvin KM,
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Curtis RAJ, Olandt PJ, Tsai F,
Silos-Santiago I, Bandaru R;
                                                 99US-00163821.
99US-0117580P.
99US-00276400.
99US-00365162.
99US-00392189.
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2000US-0234922P.
2000US-0236595P.
2000US-0246669P.
2000US-0248325P.
2000US-0248832P.
2000US-0248831P.
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2001US-00945044.
2001US-00909743.
2001US-00909743.
2001US-00929346.
2001US-00929218.
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99US-00448076.
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2001US-00963159
2001US-00008016
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2003US-00336489
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25-APR-2003; 2003US-00423543
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differentiative disorders, brain disorders, platelet disorders, breast disorders, breast disorders, brain disorders, platelet disorders, breast disorders, brain disorders, lung disorders, breast disorders, brond disorders, kidney (renal) disorders, lung disorders, prostate disorders, lung disorders, prostate disorders, lung disorders, prostate disorders, cervical disorders, spleen of disorders, prostate disorders, restes disorders, spleen conduction disorders, pancreatic disorders, skeletal muscle disorders, cervical disorders, pancreatic disorders, restes disorders, cervical disorders, manuel, e.g. inflammatory disorders, cardiovascular disorders, candothelial cell disorders, luver disorders, viral diseases, pain disorders, metabolic disorders, blood vessel disorders or angiogenic disorders, exphroid disorders, blood vessel disorders or angiogenic disorders (all claimed), e.g. cancer, heart failure, hypertension, angina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease psoriasis, or asthma. The nucleic acid molecules and colypeptides are also useful as modulating agence in regulating a variety of cellular process, e.g. cell proliferation, differentiation, growth and division. This sequence encodes a novel human protein of the invention. Colerthonic format from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             electronic format from
ftp.seqdata.uspto.gov/sequence.html?DocID=20040058355.
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Sequence 1884 BP; 403 A; 599 C; 548 G; 334 T; 0 U; 0 Other;

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The present invention relates to the isolation of a novel human protein kinase designated 3700, and the polymucleotide sequence encoding it. The invention also describes the use of a modulator of the activity of protein kinase (PK) 3700 for making a medicament or pharmaceutical composition for modulating the ability of a cell to phosphorylate an amino acid residue of a subservate protein. Modulators of protein kinase 3700 activity are useful for modulating protein phosphorylation, cell signalling, tumourigenesis, mitogenesis, transcription of a gene, and signalling, tumourigenesis, mitogenesis, transcription of a gene, and signalling, tumourigenesis, and signalling across the blood-brain barrier. The polymucleotide and polypeptide molecules for protein kinase parrier. The polymucleotide and polypeptide molecules for protein kinase prognosticating, diagnostic targets and therapeutic agents for prognosticating, diagnostic targets and therapeutic agents for prognosticating, diagnosting, preventing, inhibiting, alleviating, or prognosticating, diagnosting, preventing, inhibiting, alleviating, or curing PK-related disorders and cellular proliferative and/or disorders (e.g. haematopoietic neoplastic disorders, carcinoma, sarcoma, metastatic disorders or leukaemia). The 3700 to polynucleotide sequence can be used to express protein kinase 3700, to detect a genetic alteration in a 3700 gene, in chromosome mapping, for
GAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTTTCCCTGACAG 1825
                                                                                                                                                                                                                                                                                                                                                         Human; protein kinase 3700; PK; protein phosphorylation; tumourigenesis; cell signalling; mitogenesis; gene transcription; angiogenesis; sarcoma; cissue repair; tissue regeneration; atheroselerosis; blood-brain barrier; cell proliferation disorder; cell differentiation disorder; carcinoma; haematopoietic neoplastic disorder; metastatic disorder; leukaemia;
                                     ACTGCCAAGAGGTGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC 1893
                                                             157. .2043
/*tag= a
/*product= "Protein kinase 3700"
/product= "The coding region (not including the terminator codon) is specifically claimed in claims 7 and 28"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of modulators of activity of 3700 protein for making medicament se.g., modulating protein phosphorylation or cell signaling, or for treating or preventing cellular proliferative and/or differentiative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; antiatherosclerotic; gene; ss
                                                                                                                                                                                                                                                                                                                 encoding human protein kinase 3700
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                                                                                                                                                                                       ABK14000 standard; cDNA; 3353
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                                                                                                                                                                                                                                                                         (first entry)
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P-PSDB; AAU79652.
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 surrogate markers. The present
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                                                                                                                                          CCTCCGCCCTGGCCTCGGAGAGCGCCCGGCCGCTGGCGGACGGGCTCATCAAGTCGCCTA
                                                                                                                                                                       ccacrecercegececagageragecegecegecegesegeaaggereareagececa
                                                                                                                                                                                                      107 AACCTCTGATGAAGAAGCAGGGGGTGAAGCGGCACCATCACAAACACAACCTGCGGCACC
                                                                                                                                                                                                                                   AGCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACCACCACAACCTGCGGCACC
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                                                                                                           21;
                                               T; 0 U; 3 Other;
                                                                          9
                                                                                                           273;
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                                             Sequence 3353 BP; 754 A; 1022 C; 879 G; 695
tissue typing, in forensic biology, and as sequence encodes human protein kinase 3700
                                                                          Score 1360.2;
Pred. No. 0;
                                                                                                           0; Mismatches
                                                                            71.9%;
84.2%;
                                                                                                           Conservative
                                                                         Query Match
Rest Local Similarity
                                                                                           Best Local Sim:
Matches 1565;
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pain disorder;
            angiogenesis inhibitor; angiogenesis stimulator; cerebroprotective; nephrotropic; antithyroid; dermatological; immunomodulator; celebroprotective; nephrotropic; antithyroid; dermatological; immunomodulator; nephrotropic; antithyroid; dermatological; immunomodulator; brain disorder; platelet disorder; lorast disorder; colon disorder; kidney disorder; renal disorder; lung disorder; ovarian disorder; thyroid disorder; testes disorder; haematopoietic disorder; thymus disorder; pancreatic disorder; skeletal muscle disorder; skeletal muscle disorder; skeletal muscle disorder; immune disorder; inflammatory disorder; cardiovascular disorder; endothelial cell disorder; disorder; immune disorder; metabolic disorder; neinflammatoric disorder; nein
                                                                                                                                                                                                                                                                                  multiple sclerosis; Crohn's disease; psoriasis; asthma; cell proliferation; cell differentiation; cell growth; cell division;
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Chun M, Williamson MJ;
                                                                                                                                                                                                                         metabolic disorder; neurological disorder;
central nervous system disorder; erythroid disorder;
blood vessel disorder; angiogenic disorder; cancer; heart fe
hypertension; angina; osteoarthritis; rheumatoid arthritis;
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   antipsoriatic; antiasthmatic; cardiovascular;
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Curtis RAJ, Olandt PJ, Tsai F,
Silos-Santiago I, Bandaru R;
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990S-01076400
990S-00395162-
990S-00395189-
990S-00412210
2000US-01860TF-
2000US-018688P-
2000US-0206888P-
2000US-020688P-
2000US-020688P-
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2000US-0248325P
2000US-0248312F
2001US-026166P
2001US-00797039
2001US-00909743
2001US-00909743
2001US-0092918
2001US-00929218
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2001US-00929218
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2002US-00217168.
2002US-00278036.
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2001US-00003690.
2002US-00060763.
2002US-00105989.
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2000US-0235035P
2000US-0246669P
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22-DEC-2000;
05-JAN-2001;
28-FEB-2001;
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25-SEP-2001;
08-NOV-2001;
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12-AUG-2002;
22-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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09-SEP-1999;
05-OCT-1999;
23-NOV-1999;
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14-AUG-2001;
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25-MAR-1999
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                      GCTTCTTCAAGCAGCACGTGCCGGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGCCAAC 1126
                                                                                                                                         ATTCTCTTAAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATCTGCAAGGTGACCCGG 1186
                                                                                                                                                                                                                                                                                      AGAAAAAGTCCTCTACCTCGTCAGGGGAGGTACAGGAGGACCCTCAGGAACTCAGACCGG 1306
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                                                                                          TGGCGGACTGGTTACGTCGCTCCTCGCGCCCCCTCGGAGAATGGAGCCAAGGTGTGCA
                                                                                                                                                                            ATTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCCAGTCTCTCCACAGAGACACGG
                                                                                                                                                                                                              CTGAGGATACCTCTTCTCGCCCTGGCAAGAGCAGCCTTAAAGCTTCCGAAAGGCATTCTCA
                                                                                                                                                                                                                                                   CTGATGACACTGCCCATCGCCTGGCAAGAGCAACCTCAAGCTGCCAAAGGGCCATTCTCA
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2004-268788/25 WPI; 2004-268788/ P-PSDB; ADL14161

New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecules and proteins, useful for treating, e.g. cancer, failure and angina.

Claim 1; SEQ ID NO 43; 139pp; English

The invention describes an isolated 21910, 56634, 55053, 2504, 15977, 21970, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising any one of 40 nucleotide sequences (I). The nucleic acid molecules and colypeptides are useful for diagnosing and treating a subject having a disorder, which is associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501, 26733, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, associated with aberrant 21910, 56634, 18610, 33217, 21967, h1983, associated with aberrant 21910, 56634, 18610, 33217, 21967, h1983, associated with aberrant 21910, 56634, 18610, 33217, 21967, h1983, associates, prostate disorders, kidney (renal) disorders, kidney (renal) disorders, kidney (renal) disorders, prostate disorders, kellog disorders, cavarian disorders, pancreatic disorders, testes disorders, candothelial disorders, disorders, cardiovascular disorders, pancreatic disorders, skeletal muscle disorders, disorders, associated with bone metabolism, candothelial cell disorders, liver disorders, viral diseases, pain disorders, metabolic disorders, necrological or central nervous system disorders, metabolic disorders, blood vessel disorders or angiogenic disorders, metabolic disorders, blood vessel disorders or angiogenic disorders, explainties, rheumatoid arthritis, multiple sclerosis, cronce, angina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, cronce, angina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, collibration, growth and division. This sequence encodes a novel human protein of the invention. The sequence encodes a novel human protein of the invention. Soletions of cellular process, e.g. cellular p ftp.seqdata.uspto.gov/sequence.html?DocID=20040058355 electronic format

Sequence 3353 BP; 754 A; 1022 C; 879 G; 695 T; 0 U; 3 Other;

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166 310 CCACTCCCTCGGCCGCAGAGCTAGCCCGGCCGCTGGCGGAAGGCCTGATCAAGTCGCCCA 250 AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACA 346 TCATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATG 406 610 CCTCCGCCCTGGCCTCGGAGAGCGCCCCGGCCGCTGGCGGACGGGCTCATCAAGTCGCCTA TCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTGATCGTCATGGAGTATG AACCTCTGATGAAGAAGCAGGCGGTGAAGCGGCACCATCACAAACACAACCTGCGGGCACC **AGCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAGCACAACCTGCGGCACC** GCTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAAGGCACGAG AGAGCTCGGGGCGTCTGGTGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGC CCAGCCGAGGCGATCTGTATGATTACATCAGTGAGCGGCCACGGCTGAGCGGGACG ccaecceaeceaecerrareaeraearcaeceaeceaecaecreaeraeceaeae Gaps Score 1360.2; DB 12; Length 3353; Pred. No. 0; 0; Mismatches 273; Indels 21; C Query Match
Best Local Similarity 84.2%;
Matches 1565; Conservative 191 251 167 227 47 107 311 371 287 431 347 491 407 551

1390 1186 1330 1246 1546 1006 1210 1126 1270 1366 1426 1486 1030 1090 1066 AGAAAAAGTCCTCTACCTCGTCAGGGGAGGTACAGGAGGACCCTCAGGAACTCAGACCGG 1306 AGAAGAAGGTGTCAGCCTCTGCAGAAGGGGTACAGGAGGACCCTCCGGAGCTCAGCCCAA 1450 1501 1561 1621 1681 1547 CCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCT 1606 586 646 910 886 946 670 730 790 706 850 996 826 970 GCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACCCTGGCCTGGAGGCCACC CCAGGCATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACTGCCACCAGAACGGGATCG CTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGCCATCAGAACAGAGTTG TTCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG rccacceagarcrcaagcregagaacarccrcrrggareccaareegaararcaagarre CTGACTTTGGCCTCTCCAACCTGTACCACAAGGCAAGTTCCTCCAGACGTTCTGTGGGGA creacricescercreaecercracearcaaeceaecreerscaecarrereresea GCCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCCAGAGGTGG GCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTACACAGGCCCAGAGGTGG ACAGCTGGTCTCTGGGCGTTCTCCTGTACATCCTGGTGCATGGCACCATGCCCTTTGACG ACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGCACCATGCCCTTTGATG GGCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGGCTTACCGTGAGCCGCCCA GGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCCTTACCGGGGGCCCTA AGCCGTCCGATGCCTGTGGCCTGATCCGGTGGCTGTTAATGGTGAACCCCCACCCGTCGGG CCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAACTGGGGTTACACCACCGCAGTCG .031 ccacccrecadarereccaercacrecaerecaereaerececeraceccaeceaeree GGGAACAGGAAGCCCTGCGTGAGGGTGGGCACCCTAGTGGTGACTTTGGCCGGGCCTCCA GAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCCTGGCAGTGACTCTGCCCGCGCCTCCA GCTTCTTCAAGCAGCACGTGCCGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGGCAAC ATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATCTGCAAGGTGACCCGG CTGAGGATACCTCTTCTCGCCTGGCAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCA TGCCTGATACTCCAGGGCAGCCTGTCCCTGCTGTATCCCTGCTCCCAAGGAAAGGCATCC TCCCTGCGAGCCCAGGCCAGGCTGCCC-----CCCTGCTCCCCAAGAAGGGCATTC TTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCCTCCTCCAGAGCCCAGCGAGTCTG GGGAACTCTTAGACGCCAGTGATGTTTTGTGAGTGGGGACCCCGTGGAGCAGAAGTCTC GGGAGCTCTTGGACGCAGGCGTGTTTGTGAGTGGGGATCCCCAAGGAGCAGAAGCCTC CACAGGCTTCAGGGCTCCTCCTCCACCGCAAGGGCATTCTCAAACTCAATGGCAAGTTCT TGGCGGACTGGTTACGTCGCTCCTCGCGCCCCTCCTGGAGATGGAGCCAAGGTGTGCA cecaagerrcaegecrecrecrecarecaaagecarecreaaacreaargecaagrrer 671 731 647 791 707 827 971 1001 1001 1067 1211 1271 1187 1331 1247 1391 1307 1367 1502 1427 1562 1487 167 611 527 587 851 767 911 887 947 1127 1451 a ò 셤 ò 셤 ò g ð 셤 8 엄 ð 유 ò 원 ò g ð g ð 셤 à 요 ò 셤 ð g ò 엄 8 g à 셤 ò g ò $\ddot{\Xi}$

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WPI; 2002-090207/12. P-PSDB; AAE16266.

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TGTCCTCCGAGTCCTTTGACCAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCACTGA 1726
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Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;
Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
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30-JUN-2000;
07-JUL-2000;
13-JUL-2000;
25-AUG-2000;
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                                                                                                         New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.
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Best Local Similarity 83.7%; Pred. No. 0;
Matches 1569; Conservative 0; Mismatches 284; Indels 21;
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	RESULT 7 AAK94280 ID AAK94280 standard; cDNA; 3395 BP. XX AC AAK94280; XX DT 06-NOV-2001 (first entry)		PN EP1130034-AZ. XX	XX		P-FSUB; AAM93380. 830 Primers useful for synthesizin genetic manipulation.	XX XX C The invention relates to primers for synthesising full length CDNA C Clones. 830 CDNA molecules encoding a human protein have been isolated C clones. 830 CDNA molecules encoding a human protein have been isolated CC and nucleotide sequences of 5' - and 3'-ends of the cDNA molecules have CC been determined. Primers for synthesising the full length cDNA are useful C for clarifying the function of the protein encoded by the CDNA. The full CC length clones were obtained by construction of full length enriched CDNA CC increase that were synthesised by the oligo-capping method. The primers C mable the production of the full length human cDNA of the CC methods. The present sequence is a full length human cDNA of the CC invention. Note: The sequence data for this patent did not form part of CC the printed specification, but was obtained in CD-ROM format directly CC from EPO
S12 ACCAGAACGGGATCGTTCACCGGAATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATG	Qy 872 ACCCCACCCGTCGGGCCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAACTGGGGTT 931 Db 938 ACCCCACCCGCGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGGGGCT 997 Qy 932 ACACCACCGGAGTCGGGAACAGGAAGCCCTGCGTGAGGTGGGCTGGGCTACTGCTGATT Pl	992 TTGGCCGGCCTCCATGGCGGACTGGTTACGTCGCTCCTCGGCCCCCTCCTGGAGATG	DD IIIB GGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACCCCTG 1177 OY 1112 GGCTGGAGCGCCAACATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATC 1171 DD 1178 GCCTGGAGCGCCAGCATTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCAGTCTC 1237	OY 1172 TGCAAGGTGACCCGGCTGAGGATACCTCTCGCCCTGGCAAGAGCGAGC	2 CGAAAGGCATTCTCAAGAAAAAGTCTCTACCTCGTCAGGGGAGGTACAGGAGGACCCTC	1352 CAAGGAAAGGCATCCTTAAGAAGTCTCGACAGGCAGGATCTGGTTACTACTCCTC 1352 CAAGGAAAGGCATCCTTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCCTC 1409 CCAAGAAGGGCATTCTCAAGAAGCCCCCGACAGCGCGCGAGTCTGGGTTACTACTCCTC	Oy 1412 AGCCCAGCAACTCTGGGGAACTCTTAGACGCCAGTGATGTTTGTGAGTGGGGACCCG 1471 Db 1469 AGCCCAGTGAATCTGGGGAGCTCTTGGAGGCGACGTGTTTGTGAGTGGGATCCCA 1528 Oy 1472 TGGAGCAGAAGTCTCCACAGGCTCCTCCTCCACCGCAAGGGATTCTCAAAC 1531 Oy 1529 AGGAGCAGAAGCTTCAGGGCTCCTCCTCCATCGCAAGGGATTCTCCAAAC 1531 Db 1529 AGGAGCAGAAGCTCTCCCGCAAGCTTCTCCTCAAAC 1588 Oy 1532 TCAATGGCAAAGCTCTCCCGAAGCTTAGAAGGACTTCGCCTCAAAC 1589 Db 1589 TCAATGGCAAGTTCTCCCAAGACTTGGAGCTTCGCGCCCCCACCACCTCGGGCTTCGGCTCCC 1648 Oy 1592 TGGACCAACTGGCCTCCTCCCAACCCTCGCACCCCCCCCACAGGGCTGTGA 1651

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& a	47 CCTCCGCCCTGGCCTCGGAGAGCGCCCGGCCGCTGGCGGACCTCATCAAGTCGCCTA 106	-	ATTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCAGTCTCTCCCACAGTGACACGG 1291
D O	107 AACCTCTGATGAAGAAGAGGGGGGACCATCACAAACACAACCTGGGGACC 166 	oy Db	1187 CTGAGGATACCTTCTCGCCCTGGCAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCA 1246
& 8	167 GCTACGAGTTCCTGGAGACGCTGGGCAAGGCACCTACGGGAAGGTGAAGGCCACGAG 226	Cy Dp	1247 AGAAAAGTCCTCTACCTCGTCAGGGGAGGTACAGGAGGACCCTCAGGAACTCAGACCGG 1306
è 8	AGAGCTCGGGGCGTCTGGTGGCCATCAGGAAAAAAAAAA	da da	1307 TGCCTGATACTCCAGGGCAGCCTGTCCCTGCTGTTCCCTGCTCCCAAGAAGGCATCC 1366
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λο QΩ		oy Oy	1427 GGGAACTCTTAGACGCCAGTGATGTGTTGTGAGTGGGGACCCCGTGGAGCAGAAGTCTC 1486
<u>ک</u> ۾	CCAGCCGAGGGGATCTGTATTACATCAGTGAGGGCCACGGCTGACGGGGGCCCACGGGGGGCCACGCGGGGGGCGCCACGGGGGG	S d	1487 CACAGGCTTCAGGGCTCCTCCACCGCAAGGCATTCTCAAACTCAATGGCAAGTTCT 1546
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8 6 B	TTCACCGAGATCTCAAGCTGGAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG [જે ^વ ત	1607 CCTCCCATCTGCAGCCCGGCCCCTCAGGGGCTGTGAGTGA
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y d	GGCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGGCGCCCA 	ço, da	1835 ACTGCCAAGAGGTGACTGCAGCCTACAGACAGCCCTAGGAATCTGCTCAAAGCTCAGC 1893
کہ p	827 AGCCGTCCGATGCCTGATGCGTGGTGGTTAATGGTGAACCCGACCGGTGGG 886	RES ADL ID	ILT 8 30885 ADL30885 standard; cDNA; 3395 BP.
ò 9	887 CCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAACTGGGGTTACACCACGGAGTCG 946		ADL30885; 20-MAY-2004 (first entry)
<i>ह</i> े :	GGGAACAGGAAGCCCTGCGTGAGGTGGGCACCCTAGTGGTGACTTTGGCGGGCCTCCA		Full length human cDNA clone SeqID 2918.
g &		OS X KK KK	KW human; medicine; signal transduction; glycoprotein; transcription; KW oligo-capping method; ss; gene. XX OS Homo sapiens.

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T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3395 BP; 722 A; 1044 C; 894 G; 735 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                         Ishii S,
S, Otsuki
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                                                                                                                                                                                                                                                       Hayashi K,
K, Kojima S
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                                                                                                                                                                                                                                                         kawa T, Isogai T,
Sugiyama T, Nagai
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                                                                                                                                                               02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
                                                                                                                          99JP-00194486.
2000JP-00118774.
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P-PSDB; ADL30886.
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Matches 1563; Conserv
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11-JAN-2000;
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Score 1357; DB 12; Pred. No. 0; 0; Mismatches 275;

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CCTCCGCCCTCGGAGAGCGCCGCCGCTGGCGGACGGGGCTCATCAAGTCGCCTA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, extending and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polynucleotide sequence is a human kinase DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGATCTGATGCACATACGGAGGGAGAGTTGAGATCATGTCATCACCCTCAACCACCCTCACA
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                                                                                                                                            Seguence 3463 BP; 732 A; 1057
                                                                                                                                                                     Query Match
Best Local Similarity 84.1%;
Matches 1563; Conservative
                                                                                                                  of the invention.
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                                                                                                                                                                                                                                      cancer,
                                                                                                                  -----GICTGAAGCGATGGTGGCAGGAATCCTTGGGGGATAGCTGCTTTTCTCTGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                       gene; ds; kinase; human; SNP; single nucleotide polymorphism; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease; cardiovascular disease; brain; neuronal associated disease; metabolic; inflammatory disorder; cytostatic; neuroprotective; immunomodulator; antinflammatory; calcium/calmodulin-dependent protein kinase; NuaK2.
                                                                                                                                                                                                                                                                                                                                                                                              calcium/calmodulin-dependent protein kinase NuaK2 DNA SeqID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule encoding a kinase polypeptide, use preparing a composition for treating diseases or disorders, or neurological, immunological or inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 11; 366pp; English
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706 882 994 942 826 887 CCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAACTGGGGTTACACCACCGGAGTCG 946

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This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enzymes. The present invention describes

(first entry)

20-JAN-2003

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1366
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                                                                                                          TGGCGGACTGGTTACGTCGCTCCTCGCGCCCCTCCTGGAGAATGGAGCCAAGGTGTGCA
                                                                                                                                                                     GCTTCTTCAAGCACGTGCCGGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGGCAAC
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ABZ11333 standard; cDNA; 2043

RESULT 10 ABZ11333 ID ABZ1 XX AC ABZ1

ABZ11333

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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ1119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autoinmune diseases (multiple sclerosis, in diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
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                                                                                                                            Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermacological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders.
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Pred. No. 0;
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I Y, Yamazaki V, Chen R,
Wang D, Drmanac RT;
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05-MAR-2002; 2002WO-US005095.
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DRMANAC R
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New isolated arginine-rich protein-like polynucleotides and polypeptides, useful for diagnosing and/or treating conditions associated with aberrant activity of the arginine-rich polypeptides, such as cancer and Disclosure, SEQ ID NO 215; 51pp; English WPI; 2004-238579/22 inflammation

The invention relates to an isolated polynuclectide. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of the arguine-rich protein-like polypeptides, such as mapping, identification of mutations responsible for genetic disorders, and in assessing biodiversity. The present sequence represents a novel human arguine-rich protein CDNA.

Sequence 2501 BP; 525 A; 788 C; 728 G; 460 T; 0 U; 0 Other;

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2 226 286 AGAGCTCGGGGCCCTGGTGGCCATCAAGTCAGGAAGGACAAAATCAAAAGATGAGC 379 346 CCTCCGCCCTGGCCTCGGAGAGCGCCCGGCCGCTGGCGGACGGGCTCATCAAGTCGCCTA 106 CCACTCCCTCGGCCGCAGAGCTAGCCCGGCCGCTGGAAGGGCTGATCAAGTCGCCCA 199 AACCTCTGATGAAGAAGCAGGGGGGGCACCATCACAAACACACAGGGGCACC 166 259 GCTACGAGTTCCTGGAGACCCTGGGCAAAGGCACCTACGGGAAGGTGAAGAGGCGCGCGG 319 TCATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATG 406 499 466 559 CCAGGCATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACTGCCACCAGAACGGGATCG 526 619 586 679 646 739 706 799 296 859 GGCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCCGCCCA 826 GCCCCCTCTATGCCTCGCCAGAGATTGTCATGGGAAGCCCTACACAGGCCCAGAGGTGG rccacceagarcrcaagcregagaacarccrcrregareccaaregeaararcaagarre AGCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAGCACCTGCGGCACC GCTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAGCACGAG AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGC AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCACA rcarrectargaagrerrrgagaagaagaagaagarcgrgarcgrgagararg CAGCCGGCGACCTTTATGACTACATCAGCGAGCGCAGCAGCTCAGTGAGCGCGAAG TTCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG CTGACTTTGGCCTCTCCAAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGA GCCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGGCCCAGAGGTGG ACAGCTGGTCTCTGGGCGTTCTCCTGTACATCCTGGTGCATGGCACGTGCCCTTTGACG Gaps DB 12; Length 2501; 21; 276; Indels Score 1355.4; Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 84.0%;
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& - ₽	980	CCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAACTGGGGTTACACCACGGAGTCG 946
\$ B	947	GGGAACAGGAAGCCCTGCGTGAGGGTGGGCACCCTAGTGGTGACTTTGGCCGGGCCTCCA 1006
ò	1007	TGGCGGACTGGTTACGTCGCTCCTCGCGCCCCTCCTGGAGAATGGAGCCAAGGTGTGCA 1066
ò	9	CTTCTTCAAGCAGCACGTGCCGGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGGCAAC 112
qq	9	CTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACCCCTGGCCTGGAGCGCCAGC 121
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                                                                                                                                                                                                                                                                                                                88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Human cell cycle-associated cDNA from clone DKFZphtes3_7j3
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larity 84.0%; Pred. No. 0;
Conservative 0; Mismatches 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 942-943; 1095pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEHU-) GERMAN HUMAN GENOME PROJECT,
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                                                                                                                   ABX71420 standard; cDNA; 3443
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99US-0156503P
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Matches 1562; Conserv
                                                                                                                                                                                                                                                                                                              Human; gene; gene
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28-SEP-1999;
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in the formation, differentiation and maintenance of multicellular proteins play important roles in the formation, differentiation and maintenance of multicellular coganisme. The face of many individual cells (for example proliferation, migration or differentiation) is typically governed by information or differentiation) is typically governed by information cecived from other cells and the immediate environment. The information of received from other cells and the immediate environment. The information of factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors are paramaceutical and diagnostic agents, such and receptors or membrane bound proteins and receptors along with the cDNA sequences encoding them. The novel provides the amino acid sequences of novel human membrane bound receptors or motorion and proteins along with the cDNA sequences encoding them. The novel corrections of the invention may be the stimulation of chondrocytes. The nucleic acids of the invention may be tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is a cDNA sequence a human PRO protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rccacceaearcrcaaecresaeaacarccrcraeareccaareseaararcaaearre 701
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                                                     This invention relates to novel nucleic acids encoding human PRO secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTGATCGTCATGGAGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 276; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1355.4; DB 10;
Pred. No. 0;
SEQ ID NO 639; 918pp; English.
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84.0%;
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                                                                     GGGAGCTCTTGGACGCAGGCGAGGTGTTGTGAGTGGGGATCCCAAGGAGCAGAAGCCTC 1592
                                                                                                                                                                                                                                                                               cccagacadectrigeagercecececececentregerceregargaacreecec 1712
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                                                                                                                                                                                                                               CCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCT
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                                                                                                                            CACAGGCTTCAGGGCTCCTCCTCCACCGCAAGGGCATTCTCAAAACTCAATGGCAAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour; 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human secreted and transmembrane protein cDNA SegID 639
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, Wu TD;
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Db 227 AGAGCTCGGGGCGTCTGGGCAAAGGCACCTACGGGAAGGTGAAGAGGCGGGG 341 227 AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAGACAAAATCAAAGATGAGC 286 342 AGAGCTCGGGGCGCTTGGTGGCCATCAAGTCATCCGGAAGGACAAAATCAAAGATGAGC 401 287 AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCCCCCACA 346 402 AAGATCTGATGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCCCCCACA 461 94 TCATTGCCATCCATGAGGAGAGTTTGAGAATAGCAGATTGTCATGTCATGTCATGTGATTGTCATGTCATGTCATGTGATTGTCATGTGATTGTCATGTGATTGTCATGTGATTGTCATGGAGTATG 406 11	407 CCAGCCAAGGCATCTGTATGATTACATCAGGGGCCACGGCTGAGTGAG	S87 CTGACTTTGGCCTCTCCAACCTGTACCACAAAGCAAGTTCCTCCAGACGTTCTGTGGGA 646		1127

647 GCCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAGAGGTGG 706

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                                                                                                                              Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                                                                                                                               The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarchidis, systemic haemolyric anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating diseases of the Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polynucleotide of
                    PM,
                    Williams
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Search completed: January 24, 2005, 16:12:26 Job time : 883.636 secs

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Bird,T.A., Virca,G.D., Martin,U. and Anderson,D.M.
Bird,T.A., Virca,G.D., Martin,U. and Anderson,D.M.
Methods for identifying compounds that alter kinase activity
Patent: US 6514719-A 04-FEB-2003;
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/ John Jack Region: Serine/Threonine protein kinases, /gene="1200113B2ZRik"
// John Jack Region: Serine/Threonine protein kinases, catalytic domain. Phosphotransferases of the serine or threonine-specific kinase subfamily. The enzymatic activity of these protein kinases is controlled by phosphorylation of specific residues in the activation segment of the catalytic domain, sometimes combined with reversible conformational changes in the C-terminal autoregulatory tail."
           LKLNGKFSRTALEGTTPSTFGSLDQLASSHPAARPSRPSGAVSEDS1LSSESFDQLDL
PERLPETPLRGCVSVDNLRGLEQPPSEGLKRWWQESLGDSCFSLTDCQEVTAAYRQAL
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                                                                                        misc feature
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Matches 1880;
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RETSIMSSLAHPH I ALIHEVBRNSKT VIVMEYASRGDIJYDY ISERPRISERDARHF
RQIVSALHYCHQNGIVHRDLKLENILLDANGNIKIADPGLSNLYHKGKFLQTFCGSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be found
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitling, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzywinski, M. L., Skalska, U., Sanius, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A. Ghent, J. Schein, J. E., Jones, S. J. and Marra, M. A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 40 Row: d Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27229181.
Location/Qualifiers
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Submitted (26-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunazarne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="MGC:30598 IMM62366535655"
/tisgue_type="Mammary tumor metastatized to lung.
MMTV-LITE/Wnt1 model. Expression driven by an MMTV-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
MNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                      human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 2938)

Ralusberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altebrul, S.F., Zeeberg, B., Butcow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haich, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Scheetz, T.E., Manlek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Schenkes, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M. A. Genen, E.D., Long A. Marca, M.M. acming, S.J. and Marra, M.A. Schein, J.E., States, J. Sand, Marra, M.A. Genen, E.D., Myers, M. M. Madan, A., Schein, J. Skalska, U., Sanilus, D.E., Schnerch, A., Schein, J.E., Sanilus, J. Shalska, U., Smailus, D.E., Schnerth, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,B., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27229181.
                                                                                                                                                 ROD 04-NOV-2003
clone MGC:61244
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Submitted (13-FB2-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                         2938 bp mRNA linear Mus musculus RIKEN cDNA 1200013B22 gene, mRNA (cDNA IMAGE:6816569), complete cds.
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        1941 AGACAAGCCCTAGGAATCTGCTCGAAGCTCAGC 1973
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/organism="Mus musculus"
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ESFDQLDLPERLLETTPLRGCVSVDNLRGLEOPPSEGLKRWWQESIGDSCFSLTDCGEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="S_TKG; Region: Serine/Threonine protein kinases, catalytic domain. Phosphotransferases of the serine or threonine-specific kinases subfamily. The enzymatic activity of these protein kinases is controlled by phosphorylation of specific residues in the activation segment of the catalytic domain, sometimes combined with reversible conformational changes in the C-terminal autoregulatory tail"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGCAGGATCTGCTGCTGCAC
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                        /codon_start=1
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                                                 note="Vector: pYX-ASC"
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477 CAGAMOTTICCAGAGGCTTCAGGGCTCTCCACCGCAGGGCATTCTCAAACTCTTCATTCA	Qy Dp	oy og	O Pp	γο dα	oy Og	ò a	o, d	& 8 &	3 G (중 옵	& 8	ý g	ò q	& 8	ò a	çy d	Qy Dp	රු සි	ò
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	121 AAGCAGGGGGAAAGCGGCACCATCACAAACACAACCTGGGGCACCGCTACGAGTTCCTG 180 	181 GAGACGCTGGGCAAGGCACCTACGGGAAGGTGAAGAAGGCACGAGAGAGCTCGGGGCGT 240 	241 CTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGGATCGGTGCAC 300 	301 ATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACATCATTGCCATCAT 360 	361 GAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATGCCAGCCGAGGCGAT 420	421 CTGTATGATTACATCAGTGAGCGGCCACGGCTGAGTGAGCGGGACGCCAGGCATTTCTTC 480	481 CGACAGATCGTGTCTGCCCTGCACTACTGCCACCAGAACGGGATCGTTCACCGAGATCTC 540	541 AAGCTGGAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCTC 600 	601 TCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGAGCCCTCTCTAGGC 660	661 TCGCCTGAGATAGTCAAAGGGGAAGCCCTATGTGGGCCCAGAGGTGGACAGCTGGTCTG 720 	721 GCGTTCTCCTGTACATCCTGGTGCATGGCATGGCCCTTTGACGGGCAGGATCATAAA 780	781 ACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCCGCCCAAGCCGTCCGATGCC 840	841 IGTGGCCTGATCCGGTGGCTGTTAATGGTGAACCCCACCCGTCGGGCCACACTGGAGGAT 900	901 GTAGCCAGTCATTGGTGGGTCAACTGGGGTTACACCACCGGAGTCGGGGAAACCCGAAGCC 960 	961 CTGCGTGAGGGGGCCCCTAGTGGTGACTTTGGCCGGGCCTCCATGGCGGACTGGTTA 1020	1021 CGTCGCTCCTCGCGCCCCTCCTGGAGAATGGAGCCAAGGTGTGCAGCTTCTTCAAGCAG 1080	1081 CACGTGCCGGGAGGTGGAACTGTACCTGGGCTGGAGCGGCAACATTCTCTTAAGAAG 1140	1141 TCCCGAAAGAAATGACATGGCTCAAAATCTGCAAGGTGACCGGCTGAGGATACCTCT 1200
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1223 TCCCGCAAGGAGAATGACATGGCTCAGACTCTGCAGAATGACCCCAGTTGAAGATACTTCC 1282
                                                                                     1283 TCTCGCCCTGGCAAGAACAGCCTCAAGCTTCCGAAAGGTATCCTCAAGAAAAAGGCCTCT 1342
                                                                                                                                                          1261 ACCTCGTCAGGGGAGGTACAGGAGGACCCTCAGGAACTCAGACCGGTGCCTGATACTCCA 1320
                                                                                                                                                                                     GGGCAGCCTGTCCCTGCTGTATCCCTGCTCCCAAGGAAAGGCATCCTTAAGAAGTCTCGA 1380
                                                                                                                                                                                                                                                                                                 CAGCGTGAATCTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGAC 1440
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGGTGATGTGTTTGTGAGTGGGGACCCCGTGGAGCAGAAGTCTCCACAAGCTTCAGGG
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Rattus norvegicus (Norway rat)
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Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Daviland, C., Denson, S., Derano, C., Ding, Y., Dinh, H., Divya, K., Dragland, M. L., Denson, S., Derano, C., Ding, Y., Dinh, H., Divya, K., Dragland, M. L., Derano, S., Derano, C., Ding, Y., Dinh, H., Divya, K., Dragland, M., Derano, C., Ding, Y., Dinh, H., Divya, K., Braglan, A., Escotto, M., Sugene, C., Evans, C.A., Falls, T., Fan G., France, C., M., Garcia, A., Garcia, T., Garza, M., Gabregeorgis, B., Gerra, K., Garcia, A., Garcia, T., Garza, M., Gabregeorgis, E., Gerra, K., Gill, R., Grady, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Gabrera, M., Gabregeorgis, E., Gerrandez, P., Hanland, M., Hanl, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Haladu, S., Hune, J., Idebird, D., Jackson, A., Jackson, L., Jang, H., Johnson, R., Johnson, R., Johlson, R., Johlson, R., Mally, S., Kally, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Longon, R., Martinez, E., Mandinez, L., Liu, W., Liu, Y., London, P., Longon, R., Martinez, E., Mandinez, L., Mandinez, E., Martinez, E., Mandiney, S., McLeod, M. P., McChi, M., Malhoud, M., Maltoy, K., Martinez, E., Mandiney, S., McLeod, M. P., McChi, M., Nayu, M., Nartinez, E., Mandiney, S., McLeod, M. P., McNeill, T. Z., Menen, E., Pall, K., Mandiney, S., Mulload, P., Mandiney, S., Mulload, M., Morris, S., Munidasa, M., Murtinez, E., Pall, K., Perz, M., Perz, L., Perz, L., Perz, L., Pall, C., Pall, S., Khan, M., Reidy, R., Reilly, B., Radilly, M., Ren, Y., Reuter, M., Reidy, R., Reilly, S., Rattisber, R., Savery, G., Schere, R., William, S., Wattisber, M., Savery, G., Schere, S., Scott, G., Shateman, S., Sanders, M., Savery, G., Schere, S., Scott, G., Shateman, S., Sanders, M., Savery, G., Schere, S., Scott, G., Shateman, S., Sanders, M., Savery, G., Schere, S., Scott, G., Shateman, S., Wallber, W., Willeon, W., Willeon, W., Willeon, W., Willeon, 
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On Nov 15, 2002 this sequence version replaced gi:23269681.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the fature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
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Direct Submission
Submission
Submission
Of Wolceular and Human Geneme Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 291762)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu/
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                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                   Assembly program: Phrap; version 0.990329
Consensus quality: 226653 bases at least Q40
Consensus quality: 230853 bases at least Q30
Consensus quality: 230437 bases at least Q30
Estimated insert size: 233445; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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70377: gap of unknown length
70377: gap of unknown length
95031: contig of 24654 bp in length
108956: contig of 13825 bp in length
108056: gap of unknown length
271697: contig of 162641 bp in length
271397: gap of unknown length
273126: gap of unknown length
274531: contig of 1405 bp in length
274531: contig of 1405 bp in length
274631: gap of unknown length
274631: contig of 1656 bp in length
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contig of 1101 bp in length
gap of unknown length
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5 284658: contig of $834 bp in length
284758: gap of unknown length
9 287234: contig of 2476 bp in length
5 287334: gap of unknown length
5 291762: contig of 4428 bp in length
Location/Qualifiers
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/organism="Rattus norvegicus"
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0; Mismatches
           Center project name: GWLD
Center clone name: CH230-274J3
Project Information
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/mol_type="unassigned DNA"
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/note="Incyte ID No: 4841542CB1'
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Pred. No. 0;
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/db_xref="taxon:9606"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Primers for synthesizing full length cDNA clones and their use Patent: EP 1396543-A 2918 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers

1. 3395 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S.,

Koga, H.

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/trānslation="MESLVFARRSGPTPSAAELARPLAEGLIKSPKPLMKKQAVKRHH HANDIANFREELETLGKGTYGKVKKARBSGGRLVATKSIKKDKKKDEQDLMHIRREIE IMSSLMHPHIIAPEVERNSSKIVIVWEYASRGDLVDYISBRQOLSBEARHFRRDIY SAVHYCHQNRVVHRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASP

product"

/proteIn_id="CAF86008.1" /db_xref="GI:45502722" /note="unnamed protein /codon_start=1

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,

Homo sapiens

AUTHORS

REFERENCE

CQ782778 LOCUS DEFINITION ACCESSION VERSION VERSION SOURCE ORGANISM

RESULT 12

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DDTAHRPGKSNLKLPKGILKKKVSASAEGVQEDPPELSPIPASPGQAAPLLPKKGILK
KRRQRESGYYSSPEPSESGELLDAGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKF
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	AK074830 Homo sapiens cDNA FLJ90349 fis, clone NT2RP2003179, weakly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1). AK074830.1 G1:22760531 AK074830.1 G1:22760531 Oligo capping; fis (full insert sequence). Homo sapiens (human) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 sogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakmura, Y., Kojima, S., Nagahari, K., Mamuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K. Ninomiya, K. Ninomiya, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Otsuki, T. Direct Submission 1 sogai, T. and Otsuki, T. Direct Submission Submitted (25-MAR-2002) Takao isogai, Helix Research Institute, Genomic Baboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel.81-438-52-395; Fax:81-438-52-396) NEDO human cDNA sequencing project supported by Ministry of Genomic Submission of Medical Science, University of Institute (supported Broomy, Trade and Industry of Japan; CDNA 5:- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.). Institute of Medical Science, University of Toxyo, Laboratory of Genome Structure, Human Genome Geneer; CDNA 5:- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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                                                                                                                                                                             /note="cloning vector: pME188FL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA)
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Pred. No. 0;
0; Mismatches 275; Indels
                                                                                                                                                                                                                                                                                                         'note="unnamed protein product"
                                                       /clone="NT2RP2003179"
/cell_line="NT2"
/cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
                                                                                                                                                                                                                                                                                                                                                                          /proteIn_id="BAC11234.1"
/db_xref="GI:22760532"
   _type="mRNA"
xref="taxon:9606"
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CDNA Library Preparation: Ruthin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., E.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.L., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Straubberg N.L., Ferigold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carnindi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Maden, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and intital analysis of more than 15,000 full-length
                                                           1781 -----GTCTGAAGCGATGCTGGCAGGAATCCTTGGGGGATAGCTGCTTTTCTCTGACAG 1834
                                                                                                                             1883 GAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTTTCCCTGACAG 1942
                                                                                                                                                                                                                                                                                                                                                                                                                 BC017306 3402 bp mRNA linear PRI 29-JUN-2004 Homo sapiens likely ortholog of rat SNF1/AMP-activated protein kinase, mRNA (cDNA clone MGC:29812 IMAGE:5088037), complete cds.
1823 GGGGCTGTGTGTGTGGACAACCTCACGGGGCTTGAGGAGCCCCCCTCAGAGGGCCCTG 1882
                                                                                                                                                                                            1835 ACTGCCAAGAGGTGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC 1893
                                                                                                                                                                                                                              1943 ACTGCCAGGAGGTGACAGCGACCTACCGACAGGACTCTGCTGCTGAAAGCTCACC 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3402)
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:16878205.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                     RESULT 15
BC017306
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KEYWORDS
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TITLE

COMMENT

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DDTHARPGKSULKLFKGLKKKVSASAEGYQEDPPELLSPTPASPGQAPLLPFKKGTLK
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SQTALELAAPTTFGGLDELAPPRPLARASRPSGAVSEDS1LSSESPDQLDLPFRLPEP
PLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDPLGDSCFSLTDCQEVTATYRQALRVC
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: o Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13569921.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTCCGCCCTGGCCTCGGAGAGCGCCCGGCTGGCGGACGGGCTCATCAAGTCGCCTA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 AGAGCTCGGGGCGCCTGGTGGCCATCAAGTCCGGAAGGACAAAAATCAAAGATGAGC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 AAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTCATCACTCAACCACCCTCACA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 TCATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGC
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iive 0; Mismatches 275;
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1606 1684	1666	1726 1804	1780 1864	1834 1924	1893
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1547	1607	1667	1727	1781	1835
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Sequence 36, Appl
Sequence 1091, A
Sequence 10961, A
Sequence 237, Appl
Sequence 37, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 361, Appl
Sequence 363, Appl
Sequence 363, Appl
Sequence 363, Appl
Sequence 359, Appl
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9096.106 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1893
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                    - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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GENERAL INFORMATION:
APPLICANT: CARREFEL: SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: GRAGORIEV, IGOR
TITLE OF INVENTION: NOVEL KINASES
FILLE REFERENCE: 034536-1455
CURRENT APPLICATION NUMBER: US/10/840,512
CURRENT FILLING DATE: 2004-05-07
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Pred. No. 1.10
PRIOR APPLICATION NUMBER: 60/469,014
PRIOR FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 239
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 36
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APPLICANT: Well, Randy
APPLICANT: Miller, Barbara
APPLICANT: Meglarz, Thaddeus
APPLICANT: Gachotte, Daniel
APPLICANT: Barkealee, Beth
APPLICANT: Larrinua, Ignacio
APPLICANT: Beddy, Avutu
APPLICANT: Shukla, Vipula
APPLICANT: DW. 10852
CUGRENT PRILICANTION NUMBER: US/10/487,901
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 7560
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6208
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                                                                                                                                                                        GCTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAGGCACGAG
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Matches 457; Conservative
Matches 429; Conservative
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                                                                                                                                                                                                                                                      CGGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGCCAACATTCTCTTAAGAAGTCCCGAA 1147
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                        AGGGTGGCCACCCTAGTGGTGACTTTGGCCGGGCCTCCATGGCGGACTGGTTACGTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHAN, VIVIEN W.
APPLICANT: CARCALA, PABLO DOMINGUEZ
APPLICANT: CARCALA, PABLO DOMINGUEZ
APPLICANT: HANGEN, HONDA
APPLICANT: HANGEN, HONDA
APPLICANT: KAUFWANN, JOERG
APPLICANT: KAUFWANN, JOERG
APPLICANT: KANDAZZO, FILIPPO
APPLICANT: REINHARD, CHRISTOPH
APPLICANT: SUDDUTH-KLINGER, JULIE
TITLE OF INVENTION: IN CANDER: JO616, 900
FILE REFERENCE: 2300-21987
CURRENT FILING DATE: 2003-07-09
PRIOR FILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-06-01
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2001-02-21
PRIOR PILING DATE: 2001-03-06-03
PRIOR PILING DATE: 2001-02-04
PRIOR PILING DATE: 2001-02-04
PRIOR PILING DATE: 2001-08
PRIOR PILING DATE: 2001-12-04
PRIOR PILING DATE: 2001-12-04
PRIOR PILING DATE: 2001-02-01-08
PRIOR PILING DATE: 2001-02-01-03-01-08
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89.9%; Pred. No. 1.2e-77;
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NUMBER OF SEQ ID NOS: 13996
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10961
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Length 4094; Indela

10.4%; Score 197.4; DB 1; 54.7%; Pred. No. 1.9e-33; iive 0; Mismatches 341;

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Similarity

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CTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAGGCACGAGA cracca de a contra de contr 228 GAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGCA ccrccrcccaaggccaaggrrgcrarraaaicaragaraagaccagcrggrigaaga

217 287 347

GGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACAT

218 288 278 AAACTTGAAGAATTTTCCGGGAGGTTCAGATAATGAAGATGCTTTGCCATCCACACT CATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATGC cárcagacrictaccaggicarggagagagaggicargarrraccrigargagaaracgi

348 338 408 398 468 458 528 518 588 578 648

TAGCGGAGGGAGATATTTGACCACTTGGTAGCCCATGGAAGAATGGCAGAGGAAGCA

CAGGCATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACTGCCACAGAACGGGATCGT rcgacggaagricaaacagarcgrcacagggggggrgrrrrrgrcacagarardcgr TCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTGC TCATCGTGATTTAAAAGCCGAAAACTTACTTCTGGACGCCAATCTGAATATCAAATAGC TGACTITGGCCTCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGAG AGACTITGGCTICAGCAACCTCTTCACTCCAGGGCAGCTGCTGAAGACGTGTGTGCCAG CCCTCTTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGGCCCAGAGGTGGA 638 CCCTCCCTATGCCCCCCAGAGCTCTTCGAAGGAAGGAATATGATGGCCCAAAGTGGA CAGCTGGTCTCTGGGTTCTCCTGTACATCCTGGTGCATGGCACCATGCCCTTTGACGG CATATGGAGCCTTGGAGTTGTCCTCTATGTGCTGGTGTGTGGCGCCCTGCCGTTTGATGG

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                                                         GGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAAATCAAAGATGAGCAGGATCT 293
                                                                                                                                                                    239 AGAGAAAGTTCGCAGAGAGATTAAAATCCTGAGGTTGTTTATGCATCCACACATCATAAG 298
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GCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCCGCCCAA
                                                                                                                   828 GCCGTCCGATGCCTGTG---GCCTGATCCGGTGGCTGTTAATGGTGAACCCCACCCGTCG
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APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: GRIGORIEV, IGOR
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-1455
CURRENT APPLICATION NUMBER: US/10/840,512
CURRENT FILING DATE: 2004-05-07
PRIOR FILING DATE: 2003-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 37, Application US/10840512; GENERAL INFORMATION:
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US-10-840-512-37
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APPLICANT: SUGEN, INC.
APPLICANT: SUGEN, INC.
APPLICANT: CARNEPEEL, SEAN
APPLICANT: CHANYING, GERARD
APPLICANT: CHARYINGZAK, GJEN
APPLICANT: GRIGORIEV, IGOR
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-1454
CURRENT APPLICATION NUMBER: PCT/USO4/14421
CURRENT APPLICATION NUMBER: 60/469,014
PRIOR APPLICATION NUMBER: 60/469,014
PRIOR FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 239
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 37

LENGTH: 4094 TYPE: DNA ORGANISM: Mus musculus

Sequence 37, Application PC/TUS0414421 GENERAL INFORMATION:

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                                                                                    Length 4094;
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                                                                                    Query Match 10.4%; Score 197.4; DB 7; Best Local Similarity 54.7%; Pred. No. 1.9e-33; Matches 415; Conservative 0; Mismatches 341;
; NUMBER OF SEQ ID NOS: 239
; SCFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 4094
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-840-512-37
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134 AGCGGCACCATCACAAACACAACCTGCGGCACCGCTACGAGTTCCTGGAGACGCTGGGCA 193
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                                                        Repression
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APPLICANT: neteut_jairs, i.m.

APPLICANT: Macool, Daniel
APPLICANT: Macool, Daniel
APPLICANT: Macool, Daniel
TITLE OF INVENTION: Plant Carbon Catabolite Rep
FILE REFERENCE: B8-1315
CURRENT APPLICATION NUMBER: US/10/998,525
CURRENT FILING DATE: 2004-11-29
PRIOR FILING DATE: 2003-06-04
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
FORD SEQ ID NOS: 28
SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Zea mays
US-10-998-525-5
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RESULT 7
US-10-998-525-5
i Sequence 5, Application US/10998525
i GENERAL INFORMATION:
APPLICANT: Allen, Stephen
APPLICANT: Allen, Stephen
APPLICANT: Sakai, Hajime
APPLICANT: Weng, Zude

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TYPE: DNA
ORGANISM: Oryza sativa
US-60-638-099-214
               RESULT 9
US-60-638-099-214
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US-10-998-525-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACCCTTTGGGCGGTTACCGAATTGGCAAAACCCTAGGAATTGGGTCGTTCGGTAAAGT 83
                                                                                                                                                                        APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: Transgenic Plants with Enhanced Agronomic Phenotypes
FILE REPERBENCE: 38-21(53720)
CURRENT APPLICATION NUMBER: US/60/638,099
CURRENT FILING DATE: 2004-12-21
NUMBER OF SEQ ID NOS: 48056
SEQ ID NO 23:
LENGTH: 1512
TGTACATCCTGGTGCATGCCATGCCCTTTGACGGGCAGGATCATAAAACACTGGTGA
                          <u>irrargercircirgiescacicicestrisacearsaeaarariceaaccirrica</u>
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Pred. No. 4.6e-31;
0; Mismatches 280; Indels
                                                                                                                                                    Sequence 231, Application US/60638099 GENERAL INFORMATION:
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Similarity 56.5%;
                                                                                                                                                                                                                                                                                                                                                                           367; Conservative
                                                       AGCAPATCA 799
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                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Zea mays
US-60-638-099-231
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US-60-638-099-231
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1518;
Sequence 214, Application US/60638099
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: Transgenic Plants with Enhanced Agronomic PLIE REFERENCE: 38-21(53720)
CURRENT APPLICATION NUMBER: US/60/638,099
CURRENT FILING DATE: 2004-12-21
NUMBER OF SEQ ID NOS: 48056
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 180.2; DB 9;
Pred. No. 8.4e-30;
0; Mismatches 283;
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APPLICANT: Allen, Stephen; APPLICANT: Heppard, Elmer; APPLICANT: Sakai, Hajime
                                                                                                                                                                                                                                                                                                                                                                                                                   9.5%;
55.9%;
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Best Local Similarity 55.9
Matches 363; Conservative
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      APPLICANT: Helentjaris, Tim
APPLICANT: Macool, Daniel
APPLICANT: Macool, Daniel
APPLICANT: Macool, Daniel
TITLE OF INVENTION: Plant Carbon Catabolite Repression Proteins
FILE REFERENCE: BB-1315
CURRENT APPLICATION NUMBER: US/10/998,525
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: US/09/857,522
PRIOR APPLICATION NUMBER: US/09/857,522
PRIOR APPLICATION NUMBER: PCT/US99/29824
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 21
LENGTH: 2006
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Pred. No. 1.2e-29;
0; Mismatches 284; Indels
                                                                                                                                                                                                                                                                                                                                              9.5%;
Weng, Zude
Helentjaris, Tim
Macool, Daniel
Miao, Guo-Hua
                                                                                                                                                                                                                                                                               TYPE: DNA
CRGANISM: Triticum aestivum
US-10-998-525-21
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Best Local Similarity
Matches 363; Conserv
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RESULT 11 US-10-995-561-364

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Sequence 364, Application US/10995561
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION WIMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 364
LENGTH: 3394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 GAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGCA
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Pred. No. 1.5e-29;
1; Mismatches 352;
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Best Local Similarity 53.1%;
Matches 403; Conservative
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; ORGANISM: Homo sapiens
US-10-995-561-364
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                         Sequence 361, Application US/10995561
GREERAL INFORMATION:
APPLICANT: CARCILL, Michele et al.
APPLICANT: CARCILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 87702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 361
LENGTH: 3442
                                                                                                                                                                                                                                                                                                                                                                                 CTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAGGCACGAGA
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Pred. No. 1.5e-29;
1; Mismatches 352;
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Best Local Similarity 53.1%;
Matches 403; Conservative
                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-361
            US-10-995-561-361
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                                                                                                                                               Sequence 363, Application US/10995561
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS C
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPRENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 363
LENGTH: 3466
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1533 CGGCACTCTAGAGCAAATCATGAAGGACAGGTGGATCAA 1571
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53.1%; Pred. No. 1.5e-29;
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1; Mismatches 352;
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828 GCCGTCCGATGCCTGTG---GCCTGATCCGGTGGCTGTTAATGGTGAACCCCCGTCG
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Matches 403; Conservative
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US-10-995-561-360
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                                                                                                                                      Sequence 359, Application US/10995561
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: CENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTACGAGTTCCTGGAGGCCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAGGCACGAGA
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Pred. No. 1.5e-29;
1; Mismatches 352;
                              GGCCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAA
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ORGANISM: Homo sapiens
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LENGTH: 3487
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                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE REFERENCE: CLOUSES9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 360
LENGTH: 3514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.5e-29;
1; Mismatches 352;
                                                                                                            885 GGCCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAA
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828 GCGTCCGATGCCTGTG---GCCTGATCCGGTGGCTGTTAATGGTGAACCCCACCGTCG 884
1473 CATGTCTACAGAAACTTCTCAAACGTTTCCTGGTGCTAAATCCAATTAAAGG 1532
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Search completed: January 25, 2005, 07:13:05 Job time : 357.728 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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January 24, 2005, 14:56:28; Search time 235.428 Seconds (without alignments) 8761.524 Million cell updates/sec

Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters:

824507 seqs, 355394441 residues

Searched:

Minimum DB 8 Maximum DB 8

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:* Database

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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	B B	ΙD	Description
-	2902	100.0	2902	4	US-09-579-664B-4	Sequence 4, Appli
7	2902	100.0	2902	4	US-10-355-975A-4	
m	1372.2	47.3	2501	4	US-09-799-451-215	21.
4	202.6	7.0	2175	4	US-09-984-890-1	
ß	202.6	7.0	2175	4	US-10-274-194-1	Τ,
φ υ	189.2	6.5	484	4	US-09-270-767-1257	125
0 7	189.2	6.5	484	4	US-09-270-767-16539	Sequence 16539, A
80	186.4	6.4	2908	4	US-09-930-181-1	٦,
σ	182.4	6.3	2652	m	US-08-557-006C-39	39,
10	182.4	6.3	2761	ო	US-08-557-006C-24	24,
11	181.2	6.2	1742	m	US-08-557-006C-38	38,
12	179.8	6.2	2698	~	US-08-677-298-1	1, 7
13	176.4	6.1	2899	4	US-09-774-528-112	112
14	174	6.0	3364	4	US-09-930-181-3	m
15	173	0.9	2334	4	US-10-003-690-3	'n
16	173	0.9	2337	4	US-10-116-326-1	Sequence 1, Appli
17	173	0.9	2980	4	US-10-003-690-1	ı,
18	172.2	5.9	1539	4	US-09-633-328B-1	٦,
19	172	5.9	3609	4	US-09-799-875-6	9
20	172	5.9	5983	4	US-09-799-875-4	4
21	171.4	5.9	1647	٣	US-09-101-146-44	44,
22	165.6	5.7	1929	ᠬ	US-09-359-161-4	4,
23	163.6	5.6	1747	m	US-08-557-006C-44	44,
24	160.4	5.5	1507	4	US-09-523-849-4	Sequence 4, Appli
25	160.4	5.5	1544	4	US-09-734-673-1	1,
26	160.4	5.5	2060	4	US-09-523-849-1	1,
27	158	5.4	1736	m	US-08-557-006C-37	37.

Sequence 36, Appl	Sequence 3, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 1004, Ap	Sequence 3, Appli	Sequence 70, Appl	Sequence 138, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 1206, Ap	Sequence 1, Appli	Sequence 20, Appl	Sequence 24, Appl	Sequence 9, Appli	Sequence 1454, Ap	Sequence 5, Appli
US-08-557-006C-36	US-09-523-849-3	US-10-116-326-5	US-09-256-465-1	US-09-167-322-3	US-09-023-655-1004	US-09-590-740-3	US-09-417-197-70	US-09-417-197-138	US-09-212-771-1	US-09-091-058-1	US-09-023-655-1206	US-09-590-740-1	US-09-523-849-20	US-09-523-849-24	US-09-554-726A-9	US-09-016-434-1454	US-09-590-740-S
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1783	1051	2112	1599	1599	1599	1254	2181	2184	2610	2610	2610	2610	546	488	2738	1480	2626
5.4	5.4	5.3	5.1	5.1	5.1	5.1	5.0	5.0	2.0	5.0	0.5	5.0	4.9	4.9	4.7	4.7	4.6
158	155.6	154	149.4	149.4	149.4	147.8	144.4	144.4	144.4	144.4	144.4	144.4	143.6	143	137.6	136.2	134.6
88	29	90	31	32	33	34	35	36	37	38	33	0	41	42	43	44	52

ALIGNMENTS

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61 CCGCGGGCTCAGCGCGCGCTGCTACTGCTGCCGACCCACTCCACCTCGCGGGTCCCCGCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CCCGCGGCTCAGCGCGCGCGCTACTGCTGCCCGACCCACTCCACCTCGCGGTCCCCGCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CACTAGTGGATCCAAAGAATTCGGCACGAGGCGTGCTCGGGTGCGGCTGTGAGCTCTCTGAG
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US-09-579-664B-4

JUS-09-579-664B-4

Sequence 4, Application US/09579664B

Patent No. 6514719

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Wirca, G. Duke

APPLICANT: Wirca, G. Duke

APPLICANT: Martin, Unia

APPLICANT: Maderson, Dirk M.

TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES

FILE REPERBNCE: 2923-4

CURRENT APPLICATION NUMBER: US/09/579,664B

CURRENT APPLICATION NUMBER: US/09/579,664B

CURRENT APPLICATION NUMBER: US/09/579,664B

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 2902

TUPDE: NUMBER: 2902
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100.0%; Score 2902;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2902; Conservative 0; Mismatches
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1411 CAGGGGAGCCTGTCCCTGCTGTACTCCTCCGAAAGCAAACTCTTAAGAAGTCTTCGTGGGGAAACTCTTAG 1560 1510 CAGGGGAGCTTGGTTACTCCTCTCCGAAACCCCAGGAATTCTGGGAAACTCTTAG 1560 1510 CAGGGGGAGTTGGGGAATTCTTAG 1510 1510 CAGGGGGAGTTGGGGAATTCTTAG 1510 1510 CAGGGGGAGTTGGGGAATTCTTAG 1510 1510 CAGGGGGGGGGGGGAGTTGGGGAGTTCTAG 1510 1510 CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CCTAGTACCCAGATGCCCTGGGAAGATCGGACCGCTGTTTGACTTCATCTCAAGACGCTGCTTCATTGACTTCATCTCAAGACGCTGCTTCATCATCTCAAGACGCTGCTTTGACTTCATCTCAAGACGCTGCTTCATCATCTCAAGACTTCAAGACTTCATCAAGACTTCAAGACTTTGACTTTTTTTT
6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B	6 6 6 6
GTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATTCAAAGATGAGCAGGATCTGCTGG GTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAAATTCAAAAATGAGAACAGGAATTCTGCCACC ACATACGGAGGAGATTCAAGAATTCATCATCAACCACCCCCCACATCATTGCCATCC ACATACGGAGGAGATTCAAGAATTCATCATCAACCACCCCCCCACATCATTGCCATCC ATCAGAGTGTTTTCAATTCAA	1321 CTTCTCGCCCTGGCAAGAGCAGCTTAAGCTTCCGAAAGGCATTCTCAAGAAAAAGTCCT 1380

୍ <u>ଶ</u> ଧ		Db 2461 GGGGACCAGATGCCCCTGGACCCCATCTTAGATCTCAGAGACTTGAACCTTGAAGCTGTT 2520 Qy 2521 CCTAGTACCAGATGTGGATGGATGCTCTGTTTCTCAGGCCAACGGGACCTAGAATGTGC 2580
∂ 8	1441 CAGGCAGCCTGTCCTGTTGTTGTCCTGCTCCCAGGAAAGGCATCCTTAAGAAGTCTC 1500 	2521 CCTAGTACCCAGATGTGGATGCTCTCTCTCAGGCCAACGGGACCTAGAATGTGC
که م م	1501 GACAGCGTGAATCTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAG 1560 	Db 2581 IGACTARTIATTTTTTGTGATTCTCACTTTTTTGGTTTTTGTTTGTTTG
상 원	1561 ACGCCAGTGATGTGTTTGTGAGTGGGGACCCCGTGGAGAGAGA	Qy 2641 TITITGITTITAAGIGAATITIGCIGCTITCAATAAIGIGAATGCIGTGTTCTGGGGAAC 2700 Db 2641 TITITGITITIAAGIGAATITIGCIGCTITICAATAAIGIGAATGCIGIGTICIGGGGAAC 2700
දු පු		Oy 2701 TCCACTGTGCCACTGAAGTTTATGTACAGAGAAGTATTTGGCAATGATGCCCTCTATTC 2760 2701 TCCACTGTGCCACTGAAGTTTATGTACAGAGAAGTATTTGGCAATGATGCCCTCTATTC 2760
& g	1681 TAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCTCCTCCCATCCTG 1740 	OY 2761 AAGGGGGGTGGGGCGTTTTTCAAATGTATGTCTTGAGCACTGTCTGGATTGAGTCTCCA 2820
& g	1741 CAGCCCGGCCCAGCCGCCCTCAGGGGCTGTGAGTGGGACAGCATCCTGTCCTCCGGGT 1800 	OY 2821 GTCCCTTCACACGAGGCTGGCCACCTCCCTCATCTTCATCTGGGCCAAAAAAA 2880
<i>ò</i> ₽	1801 CCTTTGACCAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCACTGAGGGGCTGTGTGT 1860 	Qy 2881 AAAAAAAAAAAAAAA 2902
දු පු	1861 CTGTGGACAACCTGAGGGGGCTTGAGCAGCCTCCCTCAGAAGGTCTGAAGCGATGGTGGC 1920 	RESULT 3 US-09-799-451-215 ; Sequence 215, Application US/09799451
g g	1921 AGGAATCCTTGGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGCCT 1980 	; Patent No. 6783969 ; GENERAL INFORMATION: ; APPLICANT: Tang, Y. Tom ; APPLICANT: Zhou, Ping
& 8	1981 ACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAAGGGAGATGGTGCCCTAGT 2040 	; APPLICANT: Goodrich, Ryle ; APPLICANT: Asundi, Vinod ; APPLICANT: Ren, Feiyan ; APPLICANT: Zhang, Jie
& g	2041 ATGGGGTAGGCTCTGAGAGGTTTGCAGAGGAACCCTGGGTCGGATTCCTCCAGTGAATA 2100 	
ò q	2101 GAGTACATCAAGGGCTCTACGTCTGCAĆCCTGACTGAACTGA	; APPLICANT: Yamazaki, Victoria ; APPLICANT: Chen, Rui-hong ; APPLICANT: Wang, Zihwei ; APPLICANT: Wang, Dunrui
& g	2161 ATTGATGTGGAAAGGAATGGGAACCCTTGCTGCCGAGTGTTTATAGTGGGGTGGCCTGAA 2220 	/ APPLICANT: Yang, Yonghong / APPLICANT: Wehrman, Tom / APPLICANT: Ghosh, Reena / APPLICANT: Drmanac, Radoje T.
<i>જે</i> લ	2221 GGTGCCTACCTCCTTTGTGCCATGAGTGTCACCCCATGACATTTCCCACCCTGTTCTCTGG 2280 	; TITLE OF INVENTION: No. 6783969el Nucleic Acids and ; TITLE OF INVENTION: Polypeptides ; FILE REFERENCE: 803 ; CURRENT APPLICATION NUMBER: US/09/799,451
ò 8	2281 CTGCACCTTCACATAAGTTTCTGTTTCCATCAACCACCAGGGTTAGAACCCTGACTTCCT 2340 	; CURRENT FILING DATE: 2001-03-05 ; NUMBER OF SEQ ID NOS: 948 ; SOFTWARE: pt_f_genes Version 2.0 ; SEQ ID NO 215
<i>≿</i> 8	2341 GGGAGGTAATGTGTAGTGACTGCCATTATTTAGAGAGGAAACAGCCTCTGGTTTCCATCT 2400 	: LENGTH: 2501 ; TYPE: DNA ; ORGANISM: Homo sapiens ; PEATURE:
کې مځ	2401 CTGCTGCTGCATCTCAAAGACCTGGGAAGACTCGGACGCTGTTTGACTTCATCTCAA 2460 	; NAME/KEY: CDS ; LOCATION: (106)(1989) US-09-799-451-215
و	GGGGACCAGATGCCCCTGGACCCCATCTTAGATCTCAGAGCTTGAACCTTGAAGCTGTT	Query Match 47.3%; Score 1372.2; DB 4; Length 2501; Best Local Similarity 81.6%; Pred. No. 0; Matches 1649; Conservative 0; Mismatches 338; Indels 34; Gaps 4;

Qy 1162 TCCTGGAGAATGGAGCCAAGGTGTGCAGCTTCTTCAAGCAGCACGTGCCGGGAGGTGGAA 1221	Qy 1222 GCACTGTACCTGGAGCGGCAACATTCTCTTAAGAAGTCCCGAAAGGAGAATGACA 1281 	OY 1282 TGGCTCAAAATCTGCAAGGTGACCCGGCTGAGGATACCTCTTCTCGCCCTGGCAACAGCA 1341	OY 1342 GCCTTAAGCTTCCGAAAGGCATTCTCAAGAAAAGTCCTCTACCTCGTCAGGGAGGTAC 1401	Oy 1402 AGGAGGACCTCAGGAACTCAGACCGGTGCCTGATACTCCAGGCAGCCTGTCTGT	QY 1462 TATCCTGCTCCCAAGGAAAGGCATCCTTAAGAAGTCTCGACAGCGTGAATCTGGTTACT 1521	OY 1522 ACTCCTCCAGAGCCCAGGAGTCTGGGGAACTCTTAGACGCCAGTGATGTTTGTGA 1581	Qy 1582 GTGGGGACCCCTGGAGCAGAAGTCTCCACAGGCTTCACCACCACCGCAAGG 1641	Qy 1642 GCATTCTCAAACTCAATGGCAAGTTCTCCCGCACAGCCTTAGAAGGCACTACCCCTAGCA 1701	Qy 1702 CCTTTGGCTCCCTGGACCAACTGGCCTCCTCCCCATCCTGCAGCCGGCCCCGT 1761	Oy 1762 CAGGGGCTGTGAGTGAGCACAGCATCCTGTCCTCCGAGTCCTTTGACCAATTGGACTTGC 1821	Oy 1822 CTGAACGTCTTCCCGAAACCCCACTGAGGGGCTGTGTGTCTGTGGACAACCTGAGGGGGC 1881	OY 1882 TTGAGCAGCCTCCCTCAGAAGGTCTGAAGCGATGGTGGCAGGAATCCT 1929	QY 1930 TGGGGGATAGCTGTTTCTCTGACAGACTGCCAAGAGGTGACTGCGGCTACAGACAAG 1989 Db 1904 TGGGGGACAGCTGCTTTTCCCTGACAGACTGCCAGGAGGTGACAGCGACAGG 1963	OY 1990 CCCTAGGAATCTGCTCAAGCTGAGGAAGGGAGATGGTGCCCTAGTATGGGGTAG 2049	Qy 2050 GCTCTGAGAGGTTTGCAGAGGAACCCTGGGTCGGATTCCT 2090		; FACELL NIFORMATION: ; APPLICANT: YAN, Chunhua et al. ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
82 CTACTGCTGCCCGACTCCACTCGCGGTCCCCGCACCATGGAGTCGGTGGCCTTAC 141	TCAGGGCCCGAGCCAGGCTCCTCGCCTCGCCCTGGCCTCGGAGAGCGCCCGGCCGCCGCCGCCCGC	TGGCGGACGGCTCATCAAGTCGCCTAAACCTCTGATGAAGAAGCAGGGGGGGG	ACCATCACAAACACAACCTGCGGCACCGCTACCGGTTCCTGGAGCGCTGGGCAAGGGAAACCTGGGCAAGGGAAACCAAAGCAAAGCAAAGCAACGCTACGAGATTCCTGGAAACCTGGGGAAAGGCAAAGGAAAAGGAAAAGGAAAAGGAAAAGAAAAGGAAAAGAAAA	322 CCTACGGGAAGGTGAAGAAGGCACGAGAGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCA 381 	TCAGGAAAGACAAAATCAAAGATGAGCAGGATGCTGCTGCACATACGGAGGGAG	TCATGICTTCACTCACCCCCCCCACATCATTGCCATCCATGAAGTGTTTGACAATAGCA	AGTG 	AGGGCCACGGCAGGGGAAGCAGGCATAGCTACCGAAGATGGTCTGCCC 62	CTTC 68	AAAG 74	GCAAGTTCCTCCAGACGTTCTGTGGGACCCCTCTCTACGCCTCGCCTGAGATAGTCAACG	GGAAGCCCTATGTGGGCCCAGAGGTGGACAGCTGGTCTCTGGGCGTTCTCTGTACATCCTGGAAGGGGGAACAGCTGGTCTCTGGGGGTTTCTCTGTACATCCTGGAAGGGGGAACAGGTGAACAGGTGAACAGGTGAACAGGTGAACAGGTGAACAACCTACAACAACAGAAGATGAAACAACAATCCAAAAGATGGAAAGATGAAACAATCAAAAGAAGAAGAAAGA	TGGTGCATGGCACCATGCCCTTTGACGGGCAGGATCATAAACACTGGTGAAGCAAATCA 2	922 GTAACGGGGCTTACCGTGAGCCGCCAAGCCGTCCGATGCCTGTGGCCTGATCCGGTCGC 981	TGTTAATGGTGAACCCCACCCGTCGGGCCACTGGAGGATGTAGCCAGTCATTGGTGGG 	1042 TCAACTGGGGTTACACCACCGGAGTCGGGGAACAGGAAGCCCTGCGTGAGGGTGGGGACC 1101 	1102 CTAGTGGTGACTTTTGGCCGGGCCTCCATGGCGGACTGGTTACGTCGCTCCTCGCGCCCCC 1161

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Pred. No. 4e-42;
0; Mismatches 344; Indels
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001306
CURRENT APPLICATION NUMBER: US/09/984,890
CURRENT FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASLESQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2175
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Matches 422; Conservative
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US-09-984-890-1
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RESULT 5 US-10-274-194-1 Sequence 1, Application US/10274194 ; Patent No. 6706511

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APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: SCLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND ITILE OF INVENTION: THEREOF FILE REFERENCE: CL001306DIV
CURRENT PPLICATION NUMBER: US/10/274,194
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO. 1
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ORGANISM: Homo sapiens
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Score 189.2; DB 4;
Pred. No. 5.2e-39;
0; Mismatches 158;
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             64.3%;
Query Match
Best Local Similarity 64.3
Matches 284; Conservative
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US-09-930-181-1
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LENGTH: 2908
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION:
RILE REFERENCE: File Reference: 7326-094
CURRENT APPLICANT: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16539
LENGTH: 484
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                                                                          Sequence 1257, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drought REPRENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1557
LENGTH: 484
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US-09-270-767-1257
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; ORGANISM: Drosophila melanogaster
US-09-270-767-16539
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US-09-270-767-16539/c
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Patent No. 6455292
GENERAL INFORMATION:
APPLICANT: OriGene Technologies
TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
FILE REFERENCE: 16U 101 V1
CURRENT APPLICATION NUMBER: US/09/930,181
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                      CGGCCAGGAGGTGGCTATCAAAACCATCAAGAAGTGCAAGATCGAGGCCGAGGCGGATT 383
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APPLICANT: Beri, Rajindar K.
APPLICANT: Beri, Rajindar K.
APPLICANT: Beri, Rajindar K.
APPLICANT: Beri, Rajindar K.
APPLICANT: Porder, Robert A.
TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
FILE REFERENCE: NGAP/PHM37589/UST
CURRENT APPLICATION NUMBER: US/08/557,006C
CURRENT APPLICATION NUMBER: PCT/GB94/01093
PRIOR APPLICATION NUMBER: PCT/GB94/01093
PRIOR APPLICATION NUMBER: GB 9310489.1
PRIOR PLIING DATE: 1993-05-21
PRIOR FILING DATE: 1993-08-31
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver: 2.1
SEQ ID NOS: 44
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NAME/KEX: gene
LOCATION: (1)..(1747)
OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK
OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
OTHER INFORMATION: nucleide 1765
US-08-557-006C-39
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Patent No. 6258547
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Patent No. 6258547
GENERAL INFORMATION:
APPLICANT: Beri, Rajindar K.
APPLICANT: Carling, David
APPLICANT: Forder, Robert A.
TITLE OF INVENTION: WOLLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE; FILE REFERENCE: WOAPPHATSP88/UST;
CURRENT APPLICATION NUMBER: US/08/557,006C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 crgrédráriarccidiranccidirchardedeaccadaccarradadanaadaaca
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                                                                                                                                                                                                          659 TCTCAAGCTGGAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTGCTGACTTTGG
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                                                                                                      GAAGCAGGCGGTGAAGCGGCACCATCACAAACACAACCTGCGGCACCGCTACGAGTTCCT
                                                                                                                                                                                                                                                                                                                   359 GCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGCAGGATCTGCT
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                                                                                                                                                        4 GAACATGGCTGAGAAGCAGAAGCACGACGGGCGTGTGAAGATCGGACACTACGTGCTGGG
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Length 2652,
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                                                    Indele
Score 182.4; DB 3;
Pred. No. 7.4e-37;
0; Mismatches 381;
     6.3%;
                           al Similarity 53.0
437; Conservative
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     Query Match
Best Local 8
                                                       Matches
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APPLICANT: Beri, Rajindar K.
APPLICANT: Beri, Rajindar K.
APPLICANT: Carling, David
APPLICANT: Carling, David
APPLICANT: Carling, David
TILE APPLICANT: Robert Robert Robert
FILE REFERENCE: NGAP/PHM37588/UST
CURRENT APPLICATION NUMBER: US/08/557,006C
CURRENT APPLICATION NUMBER: PCT/GB94/01093
PRIOR PILING DATE: 1994-05-20
PRIOR APPLICATION NUMBER: GB 9310489.1
PRIOR PLILNG DATE: 1993-05-21
PRIOR FILING DATE: 1993-05-21
PRIOR FILING DATE: 1993-05-21
PRIOR FILING DATE: 1993-05-21
PRIOR FILING DATE: 1993-05-21
SPRIOR FILING DATE: 1993-05-21
SPRIOR FILING DATE: 1993-05-21
SPRIOR FILING DATE: 1993-05-21
SPRIOR FILING DATE: 1993-05-31
NUMBER OF SEQ ID NOS: 44
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                                                                                  800 caáagacaracagagcarcárgaargerriraaacaggarrirgccca
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Best Local Similarity 53.1%; Pred. No. 1.2e-36;
                                                                                                                                                                                                                    ; Sequence 38, Application US/08557006C; Patent No. 6258547; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human AMP protein kinase
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                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Description of Artificial Sequence: cDNA; OTHER INFORMATION: liver AMP protein kinase US-08-557-006C-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3%; Score 182.4; DB 3; Length 53.0%; Pred. No. 7.5e-37; Live 0; Mismatches 381; Indels
CURRENT FILING DATE: 1996-03-06
PRIOR APPLICATION NUMBER: PCT/GB94/01093
PRIOR FILING DATE: 1994-05-20
PRIOR APPLICATION NUMBER: GB 9310489.1
PRIOR FILING DATE: 1993-05-21
PRIOR FILING DATE: 1993-05-21
PRIOR PILING DATE: 1993-08-31
PRIOR FILING DATE: 1993-08-31
SROID NOS: 44
SOFTWARE: PATENTIN Ver: 2.1
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Matches 437; Conservative
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                                             350 GAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGCA 409
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TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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CURRENT APPLICATION NUMBER: US/09/774,528
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Patent No. 6743619
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Zhao, Qing A.
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
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Yue, Aidong J.
Tom
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Wang, Dunrui
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CGTTCTCCTGTACATCCTGGTGCATGGCACCATGCCCTTTGACGGGCAGGATCATAAAAC 904
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Patent No. 5863729
GENERAL Selection US/08677298
GENERAL Selection:
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TILLE OF INVENTION:
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SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/677,298

FILING DATE: 09-JUL-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: CATULHERS, Jennie M.

REGISTRATION NUMBER: 34,464

REFERENCE/DOCKET NUMBER: 9-96

TELEPHONE: (303) 499-8080;

TELEPHONE: (303) 499-8080;

INFORMATION FOR SEQ ID NO: 1:

SEQUIENCE CHARACTERISTICS:
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Pred. No. 3.5e-36;
0; Mismatches 352;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ilarity 53.2%;
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US-08-677-298-1
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                                                   (482) .. (2239)
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
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US-09-930-181-3
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                                                                                                                                                                                                                                                                                                                                     DB 4; Length 2899;
                                                                                                                                                                                                                                                                                                                                  Score 176.4; DB 4; Length
Pred. No. 2.7e-35;
0; Mismatches 371; Indels
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_F_genes Version 2.0
SEQ ID NO 112
LENGTH: 2899
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.4%;
Matches 412; Conservative
                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (119)..(2899)
US-09-774-528-112
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52.7%; Pred. No. 1.8e-34;
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Matches 399, Conservative
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Oy 887 CGGGCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCCGC-945

Db 696 TGACGACAACCTCCGCCAGCTGAAAGGTGAAACGGGGCTTTCCACATGCCCCA 755

Qy 946 --CCAAGCCGTCCGATGCCTGAGCCTGATGATGGTGAACCCCACCCG 1003

Db 756 CTTCATTCCTCCAGATTGCCAGACCTCCTGAGGGAATGATCGAAGTGGAGCCCGAAAA 815

Qy 1004 TCGGGCCACACTGAGGATGTAGCCAGTCATTGGTGG 1040

Db 816 AAGGCTCAGTCGGAGGATGTAGTCAGAAACATCCTTGG 852
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Search completed: January 25, 2005, 01:59:42 Job time : 241.428 secs

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January 24, 2005, 20:17:54; Search time 1516.67 Seconds (without alignments) 10994.228 Million cell updates/sec
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Listing first 45 summaries
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Sequence 22, Applisequence 1, Applisequence 21, Applisequence 21, Applisequence 27, Applisequence 43, Applisequence 25, Applisequence 25, Applisequence 215, Appliseq Sequence 4, Appl: Description 5 US-10-355-975-4 7 US-10-343-514-1 7 US-10-343-514-87 7 US-10-343-514-87 7 US-10-322-281-21 7 US-10-342-514-27 US-09-63-159-1 6 US-10-32-281-25 8 US-10-370-715B-639 8 US-10-302-175-215 SUMMARIES 四 Query Match Length 2902 3073 2929 2027 37278 2026 3353 2863.4 2066.8 2022.2 1938.8 1771.4 1379 1375.8 1375.8 1375.2

Result No.

Sequence 38, Appl Sequence 1, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 151, Appl Sequence 26, Appl Sequence 24, Appl Sequence 31, Appl Sequence 31, Appl Sequence 97, Appl Sequence 97, Appl Sequence 97, Appl Sequence 97, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 151, Appl Sequence 252, Appl Sequence 252, Appl Sequence 151, Appl Sequence 151, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 14, Appl Sequence 9, Appl Seq		Length 2902; Indels 0; Gaps 0; TGCGGCTGTGACCTCTGAG 60
US-10-311-034-38 US-09-963-159-3 US-10-423-543-45 US-10-343-514-13 US-10-343-514-13 US-10-343-514-30 US-10-343-514-31 US-10-343-514-91 US-10-343-514-92 US-10-343-514-92 US-10-343-514-95 US-10-343-514-95 US-10-343-514-95 US-10-343-514-95 US-10-343-514-96 US-10-343-514-36 US-10-343-514-36 US-10-343-514-36 US-10-343-514-36 US-10-343-514-36 US-10-343-514-14	ALIGNMENTS 355975 Al on RINE AND HUMAN KINASES 12.30 /09/579,664B	Score 2902; DB 15; Pred. No. 0; O; Mismatches 0; O; Mismatches 0; O; O; O; O; O; O; O;
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13506 1360.2 1360.	SULT 1 -10-355-975-4 bublication No. U GENERAL INFORMATI APPLICANT: BING APPLICANT: NITC APPLICANT: WITC CURRENT APPLICAT CURRENT APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION CURRENT APPLICATION PRIOR APPLICATION NUMBER OF SEQ ID SOFTWARE: PATENT SEQ ID NO 4 LENGTH: 2902 LENGTH: 2902 LTYPE: DNA ORGANISM: MUB mm CTYPE: DNA	Match Local Single 2902; 1 C . 1 C . 61 C 61 C
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	Sequence 22, Application US/1032281 Sequence 22, Application No. 1022040126762A1 APPLICANT: David W. Morris CURRENT APPLICATION NUMBER: US/10/322,281 CURRENT APPLICATION NUMBER: US/10/322,281 CURRENT APPLICATION NUMBER: US/10/322,281 SEQ ID NO 22

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                                   Score 2022.2;
Pred. No. 0;
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Best Local Similarity 99.9%;
Matches 2024; Conservative
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Sequence 87, Application US/10343514

Publication No. US20040132025A1

GENERAL INFORMATION:

APPLICANT: BRUCKER, Daniel J.

APPLICANT: ROSEN, Cheryl F.

APPLICANT: LEFEBVE, Diana L.

TILLE OF INVENTION: AMPREAELED SERINE/THREONINE KINASE, DESIGNATED SNARK

FILE REFERENCE: DPA-DRUC2/PCT

CURRENT PLILNG DATE: 2003-01-31

FRIOR PELICATION NUMBER: US/10/343,514

CURRENT PLILNG DATE: 2001-08-02

PRIOR FILING DATE: 2000-08-03

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PRIOR PLILNG DATE: 2000-08-03

PRIOR PLILNG DATE: 2001-03-12

PRIOR PLILNG DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 109

SOFTWARE: Patentin version 3.0

LENGTH: 2027

TYPE: DNA

ORGANISM: MOUSE
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GENERAL GENERAL MATCH CONTROL GENERAL STATEMENT:
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; LOCATION: (1)...(37278)
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US-10-322-281-21
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Best Local Similarity 99.9%;
Matches 1940; Conservative
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RESULT 5 US-10-322-281-21 ; Sequence 21, Application US/10322281

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JAPLICANT: DRUCKER, Daniel J.
APPLICANT: ROSEN, Cheryl F.
APPLICANT: ROSEN, Cheryl F.
TITLE OF INTURNITY EXPENDED SERINE/THREONINE KINASE, DESIGNATED SNARK
TITLE OF INVENTION: AMPR.RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REFERENCE: DPA-DRUCZ/PCT
CURRENT APPLICATION NUMBER: US 10/10/343,514
CURRENT APPLICATION NUMBER: DCT/CA01/01109
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-03-12
PRIOR APPLICATION NUMBER: US 60/222,650
PRIOR PILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
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PRIOR FILING DATE: 2001-03-14
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APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Bandaru, Rajasekhar
ITILE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
ITILE OF INVENTION: NOVEL 21910, 56634, 55053, 26176, 26139, 26176, 26131, 17TLE OF INVENTION: NOVEL 21967, h1983, m1983, 38555 OR 593 MOLECTITLE OF INVENTION: AND USES THEREFOR
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FILE REFERENCE: MPI03-0230MNIM
CURRENT FILING DATE: 2003-46-25
FRIOR APPLICATION NUMBER: US, 09/711, 216
FRIOR APPLICATION NUMBER: US, 00/205, 447
FRIOR APPLICATION NUMBER: US, 00/248, 325
FRIOR PELING DATE: 2000-11-13
FRIOR APPLICATION NUMBER: US, 10/003, 690
FRIOR APPLICATION NUMBER: US, 09/797, 039
FRIOR APPLICATION NUMBER: US, 09/797, 039
FRIOR PELING DATE: 2000-11-15
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FRIOR PELING DATE: 2000-10-28
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FRIOR PELING DATE: 2000-10-28
FRIOR APPLICATION NUMBER: US, 00/266, 061
FRIOR APPLICATION NUMBER: US, 00/248, 893
FRIOR PELING DATE: 2000-10-28
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APPLICANT: BOLDER, SARAH C.
APPLICANT: BRISDELL, HUNE
APPLICANT: APPLICANT: ARSHELL, HUNE
APPLICANT: APPLICANT: ARSHELL, HUNE
APPLICANT: APPLICANT: ARSHELL, AULL R.
APPLICANT: WILLIAMS, P. MICKEY
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TITLE OF INVENTION: Related Diseases
FILE REFERENCE: P1948RI-US
CURRENT APPLICATION NUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 639
LENGTH: 3443
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                                                  Score 1374.2; DB 18; Lengt
Pred. No. 0;
0; Mismatches 338; Indels
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Pred. No. 0;
0; Mismatches 338; Indels
                                                                                                                                         APPLICANT: WHYTE, DAVID
APPLICANT: WANNING, GERARD
APPLICANT: CARNEPEEL, SEAN
APPLICANT: CARNEPEEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: 18/10/618,941
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SEQ ID NO 11
                                          ; Sequence 11, Application US/10618941; Publication No. US20040197792A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.6%;
Matches 1651; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-618-941-11
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APPLICANT: RECIPON, Shirley A. APPLICANT: AZIMZAI, Yalda APPLICANT: DIUCKY, Jennifer L. APPLICANT: DING, Li APPLICANT: DING, Li APPLICANT: DING, Li APPLICANT: GENTHER, Megan APPLICANT: ELLIOTT, Vicki S. APPLICANT: BATRA, Sajew APPLICANT: BON, Craig H. CURRENT FILING DATE: 2002-12-10 PRIOR REPLICATION NUMBER: 60/212,073; 60/213,467; 60/216,605; 60/218,372; CURRENT FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-13; 2000- BRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/216,605; 60/218,372; CURRENT FILING DATE: 2000-06-15; 2000-06-23; 2000-07-07; 2000-07-13	- Augusta

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; Sequence 3, Application US/09963159
; Patent No. US20020077312A1
; GENERAL INFORMATION:
; APPLICAMT: Curtis, Rory A.J.
; APPLICAMT: Galvin, Katherine M.
; TITLE OF INVENTION: 3700, MOVEL HUMAN PROTEIN KINASE AND USES THEREFOR
; FILE REFERENCE: 10147-5011
; CURRENT APPLICATION NUMBER: US/09/963,159
; CURRENT PILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/234,922
; PRIOR APPLICATION NUMBER: US 60/234,922
; REGORD FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Homo sapiens
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iive 0; Mismatches
NUMBER OF SEQ ID NOS: 119
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45 ...
LENGTH: 1884
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Matches 1565; Conservative
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APPLICANT: Millennium Pharmaccuticals, Inc.
APPLICANT: Millennium Pharmaccuticals, Inc.
APPLICANT: Hunter, John J.
APPLICANT: Hanter, John J.
APPLICANT: Radolph-Owen, Laura A.
APPLICANT: Radolph-Owen, Laura A.
APPLICANT: Galvin, Kacheline M.
APPLICANT: Tasi, Forg-Ying
APPLICANT: Tasi, Forg-Ying
APPLICANT: Tasi, Forg-Ying
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Ingolada, S5051, 2504, 15977,
ITLE OF INVENTION: NOVEL 21910, 56634, 55051, 21676, 26376, 26376,
ITLE OF INVENTION: NOVEL 21910, 23004, 11083, m1983, 38555 OR 593 MOLECULES
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TITLE OF INVENTION: AND USES: 2000-40-25, 403
PRIOR APPLICATION NUMBER: US 10/219, 036
PRIOR APPLICATION NUMBER: US 60/249, 325
PRIOR PLILNG DATE: 2000-11-11
PRIOR PLILNG DATE: 2000-01-11-15
PRIOR PLILNG DATE: 2000-01-11-16
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ESFDQLDLPERLPETPLRGCVSVDNLRGLEQPPSEGLKRWWQESLGDSCPSLTDCQEV
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27229181.
                                                                                                                                                                                                                                                                                                                                                       Thomas L. Casavart.
Web site: http://genome.uiowa.edu
Web site: http://genome.uiowa.edu
Web site: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Stshier,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mote="S_TKC; Region: Serine/Threonine protein kinases, catalytic domain. Phosphotransferases of the serine or threonine-specific kinase subfamily. The enzymatic activity of these protein kinases is controlled by shosphorylation of specific residues in the activation segment of the catalytic domain, sometimes combined with reversible conformational changes in the C-terminal
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Gene, Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                           NIH-MGC Project URL: ht
Contact: MGC help desk
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Mus musculus RIKEN cDNA 1200013B22 gene, mRNA (cDNA clone MGC:61244
MAGE:6816569), complete cds.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2938)
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Contact: MGC help desk
Email: cgapba-r@mail.nih.gov
Issue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing Dy: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Villalon, D.K., Murny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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Butterfield, Y.S., Krzywinski, M. I., Skalska, U., Smailus, D.E.,
Genneration and initial analysis of more than 15,000 full-length
human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, R.S., Wagner, L., Shemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Euctow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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LKLNGKFSRTALEGTTPSTFGSLDQLASHPARPSRPSGAVSEDSILSSESFDQLDL
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6 G	2215 CCTGAAGGTGCCTACTCCTTTGTGCCATGAGTGTCACCCATGACATTTCCCACCTGTF 2274 2172 CCTGAAGGTGCCTACCTCCTTTGTGCCATGAGTGTCACCCATGACATTCCCGCCCTGTT 2231	Query N Best Lo Matches	Query Match 71.2%; Score 2066.8; DB 6; Length 2929; Best Local Similarity 86.4%; Pred. No. 0; Matches 2488; Conservative 0; Mismatches 277; Indels 115; Gaps 14	
& g	2275 CTCTGGCTGCACTTCACATAAGTTTCTGTTTCCATCAACCACGGGTTAGAACCCTGA 2334 [රු යි	49 GTGACCTCTGAGCCCGGGGCTCAGCGCGCTGCTACTGCTGCCCGACCCACCTCCACCTC 108	
රු පු	2335 CTTCCTGGGAGGTAATGTGTAGTGACTGCCATTATTTAGAGAGGAACAGCCTCTGGTTT 2394 2292 CTTCCTTGGAGGTAATGTGTAGTGACTGTCATTATTTAGAGAGAACAGCCTCTGGTTT 2351	ò a	109 GGGTCCCGCACCATGGAGTCGGTGGCCTTACTCCAGCGCCCGAGCCAGGCTCCCTCGG 168	
S G	2395 CCATCTCTGCTGCTGCATCTCAAAGACCTGGGAAGACTCGGACCGCTGTTTGACTTCA 2454	òa	169 CCTCCGCCCTGGCCTCGGAQAGCGCCCGGCCGGCGGACGGGCTCATCAAGTCGCCTA 228	
& g	2455 TCTCAAGGGACCAGATGCCCCTGGACCCCATCTTAGATCTCAGAGACTTGAACCTTGAA 2514 	<i>장</i> 점	229 AACCTCTGATGAAGAAGCAGCGGTGAAGCGGCACCATCACAAACACAACCTGCGGCACC 288	
\$ 8 8	2515 GCTGTTCCTAGTACCCAGATGTGGATGGATGCTCTGTTTCTCAGGCCAACGGGACCTAGA 2574	& A	289 GCTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAGGCACGAG 348 	
<i>\$</i> ₽	2575 AIGIGCIGACTDAITTAITTTTIGIGAITCTCACTICIGITTTTTGGITTTTGTTTGT 2634 	ò 8	349 AGACTCGGGGCGTCTGGTGGCCATCCAGCTGGAAAGACAAAATCAAGGG 408 	
S S	2635 IGITTGTTTTTGTTTTTAAGTGAATT-TTGCTGCTTTCAATAATGTGAATGCTGTGTTCT 2693 	ò 8	409 AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACA 468	
\$ 8	2694 GGGGAACTCCACTGTGCCACTGAAGTTTATGTACAGAGAAGTATTTGGCAATGATGTCCC 2753 	ò a	469 TCATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAGATTGTGATTGTCATGGAGTATG 528	
දු පු	2754 TCTATTCAAGGGGGGGGGGGGTTTTTCAAATGTATGTCTTGAGCACTGTCTGGATTGA 2813 	ò 8	529 CCAGCCGAGGCGATCTGTATGATTACATCAGTGAGCGGCCACGGCTGAGTGAG	
& g	2814 GTCTCCAGTCCCTTCACACGCCAGGCTGGCCACCCTCCTCATCTTCATCTGTGGCCAAA 2873 	රු සි	589 CCAGGCATTTCTTCCGACAGATGGTGTCTGCCCTGCACTACTGCCACCAGAACGGGATTG 648	
& 8 8	2874 AAAAAAAAAAAAAAAAAAAAAAAAA 2900 	ò a	649 TTCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG 708 609 TTCACCGGGACCTCAAGCTGGAGAACATCCTTCTAGATGCCAGTGGCAAGATCAAGATTG 668	
RESULT 4 AX380960 LOCUS DEFINITION	4 60 AX380960 2929 bp DNA linear PAT 18-WAR-2002 TION Sequence 1 from Patent WO0212456.	ò 6 ò	709 CTGACTITGGCCTCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGA 768	

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GCTTCTTCAAGCAGCACGTGCCGGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGGCAAC ATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATCTGCAAGGTGACCCGG CTGAGGATACCTCTTCTCGCCCTGGCAAGAGCACCTTAAGCTTCCGAAAGGCATTCTCA TIGAAGATACTTCCTCGCCCTGGCAAGAACAGCCTCAAGCTTCCGAAAGGTATCCTCA AGAAAAAGTCCTCTCGTCAGGGAGGTACAGGAGGACCCTCAGGAACTCAGACCGG

TTAAGAAGTCTCGACAGGGGAATCTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTG GGGAACTCTTAGACGCCAGTGATGTGTTTGTGAGTGGGGACCCCGTGGAGCAGAAGTCTC TGCCTGATACTCCAGGGCAGCCTGTCCCTGTATCCCTGCTCCCAAGGAAAGGCATCC

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6 8 6 8 6 8 6 8 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
p DNA linear PAT 18-MAR-2002 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. Affasve, D.L. 1-2002; 1 DNA"	69.7%; Score 2022.2; DB 6; Length 2027; imilarity 99.9%; Pred. No. 0; Conservative 0; Mismatches 3; Indels 0; Gaps 0; GTGACCTCTGAGCCCGCGCTCACTGCTGCCCGACCTCCTCCTC 108 GTGACTCTCTGAGCCCGCGCGCGCGCTGCTACTGCTGCCCGACCTCCTCTC 108 GTGACTCTCTGAGCCCGCGCGCGCGCGCTACTGCTGCCCGACCTCTCTCT	
AX381046 Sequence 87 from Patent W00212456. AX381046 AX381046.1 GI:19575868 Mus sp. Mus sp. Mammalia; Butheria; Rodentia; Sciurognan Drucker, D.J., Rosen, C.F. and Lefebvre, D Patent: W0 0212456-A 87 14-FEB-2002; 1149336 ONTARIO INC. (CA) Location/Qualifiers J. 2027 Mul type="unassigned DNA" //db_xref="taxon:10095"	Match Jocal Similarity 99.9%; Pred. No. 0; 19 2024; Conservative 0; Mismatches of Mis	GAGCTCGGGCGTCTGGTGGCCATCANG GGATCTGTTGCACATAGGGGGGGATT GGATCTGTTGCACATAGGGGGGGATT GGATCTGTTGCACATAGGGGGGGATT CATTGCCATCCATGAGGTGTTTGAGAAT CATTGCCATCCATGAGTGTTTGAGAAT CAGCGGGGGGATCTGTATGATTACATC CAGGCGATTTCTTCCGACAGATGTTACATC CAGGCATTTCTTCCGACAGATGGTTACATC CAGGCATTTCTTCGACAGATGGTTACATC CAGGCATTTCTTCCGACAGATCGTGCT CAGGCATTTCTTCCAGCTGGAAACATC TCACCGAGATCTCAAGCTGGAAACATC TTCACCGAGATCTCAAGCTGGAAACATC TTCACCGAGATCTCAAGCTGGAAACATC TTCACCGAGATCTCAAGCTGGAAAACATC TTCACCGAGATCTCAAGCTGGAAAACATC TTCACCGAGATCTCCAAGCTGGAAAACATC TTCACCGAGATCTCCAAGCTGGAAAACATC TTCACCGAGATCTCCAAGCTGGAAAACATC TTCACCGAGATCTCCAAGCTGGAAAACATC TTCACCGAGATCTCCAAGCTGGAAAACATC TTCACTGAGCTCTCCAACCTGTACCAC

	CTGACTITGGCCTCTCCAACCTGTACCACAAGGCAAGTTCCTCCAGACGTTCTGTGGGA [1069 GGGAACAGGAAGCCTGCGTGAGGTGAGCACCTAGTGGTGACTTTGGCCGGGCCTCCA 128 1021 GGGAACAGGAAGCCTGCGAGGGTCGCGCGCTCTA 1080 1021 GGGAACAGGAAGCTGCGAGGGTGGCCCCTCTGGCGGTGCTCTTA 1080 1129 TGGCGGACTGGTTACGTCGCTCCTCGCGCCCCCTCCTGGAGAATGGAGCCCAAGTGGTA 1140 1181
8 8 8 8 8 8	6 8 6 8 6 8 6 8 6 8 6	6 B 6 B 6 B 6 B 6 B 6 B 6 B 6
	RESULT 6 AX380986 LOCUS LOCUS DEFINITION Sequence 27 from Patent W00212456. AX380986	Querry Match 61.04; Score 1771.4; DB 6; Length 2026; Best Local Similarity 93.14; Pred. No. 0; 136; Indels 5; Gaps 3; Matches 1888; Conservative 0; Mismatches 136; Indels 5; Gaps 3; QY 99 GTGACCTCTGAGCGGGGCTCAGCGGCGCTACTCCCCGACCCCTCCGCCCC 60 GGCGTCCCGCACCATGAGCGCGCTGCTGCTGCTGCCCCCCCC

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l (Dades I to 291162).

Muzny, D. Marte., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, Y., Aoyagi, A., Aoyagi, A., Ayagi, M., Baca, E., Baden, H., Balderin, C., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bharch, C., Burch, P., Burrell, K., Calderon, E., Cardens, V., Carter, K., Casar, H., Center, A., Clavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J., Casar, H., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Coyle, M., Cree, A., Diva, M., Divya, K., Egan, A., Escotto, M., Eugene, C., Evalenic, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evalenic, C., Foster, M., Foster, P., Fraser, C.M., Gabiel, A., Ganta, R., Gardy, M., Guerre, M., Gabiel, A., Ganta, R., Gardy, M., Garner, T., Garza, M., Gabiel, A., Hadland, W., Hamil, C., Hamilton, C., Hamilton, K., Harlak, P., Hawes, A., Henderson, N., Hernandez, J., Howells, S., Huldun, S.L., Hodgson, A., Houles, S., Hladun, S.L., Hodgson, A., Houles, B., Howells, S., Hully, S., Kelly, S., Longare, S., Lopez, J., Liu, J., Liu, W., Liu, Y., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., Longacre, S., Lopez, J.,
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Rattus norvegicus clone CH230-274J3, *** SEQUENCING IN PROGRESS

***, 13 unordered pieces.
1501 GGGAACTCTTAGACGCAGGTGATGTGTTTGTGAGTGGGGACCCCGTGGAGCAGAAGTCTC 1560
                                                                                               1618 CCCGCACAGCCTTAGAAGGCACTGCCCCTAGCACTTTGGCTCCCTAGACCAACTGGCCT 1677
                                                                                                                                                                                                                                                                                                                                                        1789 TGTCCTCCGAGTCCTTTGACCAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCCACTGA 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCGATGGTGGCAGGAATCCTTGGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGG 1968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1918 TGACAGCAGCCTACAGACAAGCCCTAGGAATCTGCTCGAAGCTCAGCTGAGGAGGAGGAGG 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                       CCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCT
                                                                                                                                                                                                                                                                                                                2029 TGGTGCCCTAGT-ATGGGGTAGGCTCTGAGA-GGGTTTGCAGAGGAACC 2075
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Rattus norvegicus (Norway rat)
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SOURCE
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Submitted (02-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

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Mahashwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mahashwari, M., Mahindartne, M., Martin, K., Martinez, E.,
Mangumi, B., Mapua, P., Martin, K., Martinez, E.,
Mandiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Morris, K.,
Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pager, M., Perez, A., Perez, L., Férankoch, C.,
Plopper, F., Poindarter, A., Popovic, D., Primus, B., Du, L.-L.
Plopper, F., Poindarter, A., Rose, M., Rose, R., Riggs, F.,
Railly, B., Railly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shataman, S., Shen, H.,
Sarders, M., Savery, G., Scherer, S., Sott, C., Shataman, S., Shen, H.,
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Sneed, A., Sodergren, E., Song, X.-Z., Socrelle, R., Sosa, J.,
Sheety, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Valas, R., Vera, V., Villasan, D., Waller, R., Worley, K.,
Wang, Q., Wang, S., Wauren, R., Wei, J., Worley, K.,
Williams, G., Willson, R., Wu, J., Yakub, S., Yen, J., Yoon, L., You, E.,
Waright, D., Wirght, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoo, K.,
Waright, D., Wirght, R., Wu, J., Yakub, S., Yen, J., Yoon, L.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Smith, D. R., Holt, R.A., Smith, H.O.,
Direct Submission

AL Unpublished

Egg C., Shataman, S., Smith, D. R., Holt, R.A., Smith, R.,
E., Chang, R.,
E., Chou, M., Smith, D. R., Smith, R.,
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-helpebcm.tmc.edu
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Direct Submission
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 13 contigs. The true order of the pieces

* is not known and their order in this sequence record is

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CCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATGCCAGCC 275153
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                                                                                                   GAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTGCTGACT
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/organism="Rattus norvegicus"
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                                                               /mol_type="genomic DNA"
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/protein id="CAF86008.1"
/db.xref="G1:4550722"
/db.xref="G1:45502722"
/translation="MESLYCKRKGPTPSAAELARFLAEGLIKSPKPLMKKQAVKRHHHKMLRHRYETLETLCKGTYGKYRKARESSGRLVAIKSIRKDKIKDEOLLMHIRREIE
IMSSLMHPHIIAIHEVPENSSKIVIVMEYASRGDLYDYISERQQLSEREARHFFRQIV
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EIVNGKPYTGPEVDSWSLGVLLYILVHGTMPPDGHDHKILVKQISNGAYREPPKPSDA
CGLIRWLLMVNPTRRATLEDVASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASMAD
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DDTAHRPGKSNLKLPKGILKKKVSASABGVQEDPPELSPIPASPGQAAPLLPKKGILK
KPRQRESGYYSSPEPSESGELLDAGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKF
SQTALELAAPTTFGSLDELAPPRPLARASRPSGAVSEDSILSSESFDQLDLPERLPEP
PLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDPLGDSCFSLTDCQEVTATYRQALRVC
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTAGGAATCTGCTCAAGCTCAGCTGAGGAAGGGAGATGGTGCCCTAGTATGGGGTAG
CCTTTGGCTCCCTGGACCAACTGGCCTCCTCCCATCCTGCAGCCCGGCCCAGCCGCCCT
                                         CCTTCGGCTCCCTGGATGAACTCGCCCCACCTCGCCCCTGGCCCGGGCCAGCCCT
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RESULT 9 CQ782778

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PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI ISHII ISHII.
PI YURI KAWAI, AI WAKAWATSU, TOMOYASU SUGIYAWA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 3395)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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Primer for synthesizing full-length cDNA and use thereof FH K Location/Qualifiers

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                                                                                                                                                                                          Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2740 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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22-JAN-2002
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                                                                                                                                                                                                                                                                                                                        Query Match 47.4%; Score 1375.8; DB 6; Best Local Similarity 81.7%; Pred. No. 0; Matches 1652; Conservative 0; Mismatches 337;
1. .3395
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD127309 3395 bp DNA linear PAT 18-SEP-2002 Primer for synthesizing full-length cDNA and use thereof. BD127309 BD127309. GI:23222254 JP 2002017375-A/2740.

RESULT 10 BD127309 LOCUS DEFINITION ACCESSION VERSION KEYWORDS

us-09-980-464-4.rge

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Isogal, Helix Research Institute, na, Kisarazu, Chiba 292-0812, Japan 1:81-438-52-3986) Set supported by Ministry of Japan; cDNA full insert sequencing: chnology; cDNA library construction: University of Tokyo, Laboratory of Center; cDNA 5'- & 3'-end one pass etc.)
                                                                     CCTCCGAGTCCTTTGACCAATTGGACTTGC 1821
                                                                                                                                                GCTGTGTGTCTGTGGACAACCTGAGGGGGC 1881
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clone NT2RP2003179, weakly similar
TEIN KINASE EMK (EC 2.7.1.-).
CCCATCCTGCAGCCCGGCCCAGCCGCCCT 1761
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Sugano,S., Ishii,S.,
,J., Wakamatsu,A., Nakamura,Y.,
, Ono,T., Okano,K., Yoshikawa,Y.,
,, Okumura,K., Iwayanagi,T. and
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: o Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13569921. Location/Qualifiers
  Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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0; Mismatches 337; Indels
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/mol_type="mRNA"s"
/b xref="taxon:960"
/clone="MGC:29812_IMAGE:5088037"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SNARK"
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/db_xref="MIM:608131"
100. .1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="Lymph, lymphoma
/clone lib="NHH MGC 99"
/lab host="NH10B"
/note="Vector: pOTB7"
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Matches 1652; Conservative (
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I (bases I to 3402)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Heich, F.,
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Yillalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Voung, A.C., Shevchenko, Y.,
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TTGAGGAGCCCCCCTCAGAGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTT 1915
                                                                                      TGGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGCCTACAGACAAG 1989
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3402 bp mRNA linear PRI 29-JUN-2004 Homo sapiens likely ortholog of rat SNF1/AMP-activated protein kinase, mRNA (cDNA clone MGC:29812 IMAGE:5088037), complete cds.
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Submitted (05-NOV-2001) National Institutes of Health, Mammallan
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov/
Context: nisc.mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Becketrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
                                                                                                                                         CCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAAGGGAGATGGTGCCCTAGTATGGGGGTAG
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Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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On Aug 19, 2003 this sequence version replaced gi:16878205.
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Proc. Natl. Acad. Sci. U.S.A. 9
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TITLE
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1222 GLACTGTACCTGGGCTGGAGCGCAACATTCTCTTAAGAAGTCCCGAAAGGGAATTGCA 128 1215 GCACCACCCTGGGCTGAGGCATTCCTTCTGAAAGTCCCGCAAGGGAATTGCA 127 1282 TGGCTCAAAATCTGCAAGGCATTCCTTCTGCCTTGCCCTGGCAAGAGCA 134 1275 TGGCCCAGTCTCTCCACAGGCAAGAGCA 134 1275 TGGCCCAGTCTCTCCACAGGCTTCTCTCAGAAAAGCTTCTCCAAGAAAAGCTTCTCTCAAGAAAAGCTTCTCTCAAGAAAAGCTTCTCTCAAGAAAAGCTTCTCTCAGAAAAGCTTCTCTAAGAAAAAGCTTCTCTAAGAAAAAGCTTCTCTAAGAAAAAGCTTCTCTAAGAAAAAGCTTCTCTAAGAAAAAGCTTCTCTAAGAAAAAGCTTCTCTAAGAAAAAGCTTCTCTAAGAAAAAGCTTCTCTAAGAAAAAGCTTCTCAAGAAAAGCTTCTCTAAGAAAAAGCTTCTCTAAGAAAAAGCTTCTAAGAAAAAGCTTCTAAGAAAAAGCTTCTAAGAAAAAGCTTCTAAGAAAAAGCTTCTAAGAAAAAGCTTCTAAGAAAAAGCTTCTAAGAAAAAGCTTCTAAGAAAAAGCTTCTAAGAAAAAGCTTCTAAGAAAAAGCTTCTAAGAAAAAAGCTTCTAAGAAAAAAGCTTCTAAGAAAAAAAA	1882 TTGACGGCTCCCTCAGAAGGTCTGAAGCGGTGGGGGAATCCT 1929 1865 TTGACGGGGATCCT 1929 1866 TTGACGGGGATCCT 1929 1866 TTGAGGGGGTAGGGGCCCTCGGAAGCCTGCCGGGGGGATCCT 1925 1866 TTGAGGGGTAGGCCTCCTGGAAGCGCCTGGGGGGGATCCTT 1925 1866 GTGGGGATAGCGCTTTTCCCTGACGGCTGCCAGAGGTGACTGCCAGACAGCTTTTTTTT	RESULT 14 AX780351 LOCUS DEFINITION Sequence 2508 from Patent W003039443. ACCESSION AX780351. GI:32697345 KEYWORDS SOURCE ORGANISM Homo sapiens (human) ORGANISM Pukaryota; Metazoa; Chordata; Craniata; Wertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
142 TCCAGCGCCCGAGCCAGCCTCCCTCGCCCTCGCCTCGCAGAGCGCCCC 201 147 CGCGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	802 GGAAGCCCTATGTGGGCCCAGAGGTGGACAGCTGGTCTTGGGGCGTTCTCCTGTACATCC 861	1042 TCAACTGGGGTTACACCACCGGAGTCGGGAACCCCTGCGTGAGGGTGGGCACC 101

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Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Dugas, M., Eils, R., Brors, B. and Mergenthaler, S. Novel genetic markers for leukemias Patent: WO 03039443-A 2508 15-MAY-2003; Deutsches Krebsforschungszentrum (DE); Ludwig-Maximilian-Universitaet Muenchen (DE); PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 0;
       /gene="DKFZp434J037"
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/gene="DKFZp434J037"
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CCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAAGGAATGGTGCCCTAGTATGGGGTAG 2049
                       HSM801859 3443 bp mRNA linear PRI 20-MAR-2002
Homo sapiens mRNA; cDNA DKFZp434J037 (from clone DKFZp434J037);
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SAVHYCHQNRVVHRDLKLENIILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASP
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CGLIRWLLMVNPTRRATLEDVASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASMAD
WLRRSSRPPLLENGAKVCSFFKQHAPGGGSTTPGLERQHSLKKSRKENDMAQSLHSDTA
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PLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDPLGDSCFSLTDCQEVTATYRQALRVC
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 3443)

Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S. Direct Submission
Submitted (12-MRR-2002) MIPS, Am Klopferspitz 18a, D-82152

Martinsried, GERMANY
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Research Center (DKFZ); Email s wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the
                                                                                                                   2045 GCTCTCAGAIGCAGCTGGTIGCACCCCGAGGGAGAIGCCTIC 2087
                                                                                       2050 GCTCTGAGGGTTTGCAGAGGAACCCTGGGTCGGATTCCTCC
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/clone_lib="434 (synonym: ht
DHIOB, sites NotI + SalI"
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/note="strong similarity
protein kinases"
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

January 24, 2005, 05:56:58 ; Search time 1342.36 Seconds Run on:

(without alignments) 11348.500 Million cell updates/sec

US-09-980-464-4 Perfect score:

Sequence:

IDENTITY NUC Scoring table: 4134886 segs, 2624710521 residues Searched:

Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

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geneseqn2003ds:* geneseqn2003cs:* geneseqn2001as:*geneseqn2001bs:* genesegn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2000s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

Aac90433 Murine Ly Aad31710 Rat SNF1/ Abk14000 CDNA enco Ad114160 Novel hum Aak94280 Human ful Ad210885 Full leng Abx71420 Human cel Ad61952 Leukaemia Ad620171 Human PRO Ad96554 Human PRO Ad19655 Human pol Abx11333 Human pol Abx11333 Human pol Ad44859 Novel hum Ad14162 Novel hum Ad14162 Novel hum Ad14659 Human Kin Ad12459 Human Kin Ad12458 Human Kin Ad12337 Human TAR Abz77163 Human pro Abq72599 Human MDD Abq72698 Human MDD Description SUMMARIES ADF81952 ADO20171 ADL14162 AAF44659 ABZ77163 ABQ72599 ABQ72698 ADJ96554 ADM43851 ADL14160 ADL30885 AAC90433 AAD31710 ABK14000 ABZ11333 AAD26459 AAF75338 DB Query Match Length 2291 3200 1833 2616 2619 3353 3353 3395 3463 501 2.0444 0.022 0.024 0.025 0.034 1375.8 1375.8 1374.2 1374.2 1374.2 1374.2 1376.2 1370.6 1360.2 1349.2 1323.2 1230 849.2 849.2 Score 2902 2066 Result Š.

	Ade38420 Human pro	Adn95767 Human BEC	Adj74808 Marker ge	Adl25352 Human ARK	Adq19733 Human sof	Adp43253 Human pro	Adg23883 Human sof	Aad14328 Human pro	Aak93296 Human cDN	Aak91887 Human cDN	Ad129723 5' end of	Ad128314 5' end of	Aad03994 Human pro	Abl21269 Drosophil	Aah13802 Human cDN	Aaf44655 Novel pro	Aal60326 Human 207	Adi29353 Mouse MAR	Aba05737 Murine ne	Aba05738 Murine ne	Abs64386 Human ser	Aad51409 Human mic	Adg91747 Human mic
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17.5	17.5	17.5	17.5	17.5	17.5	17.5	17.5	17.5	12.4	12.4	12.4	12.4	12.3	10.2	9.5	8.2	8.2	8.2	8.2	8.2	8.0	9.0	8.0
507.6	507.6	507.6	507.6	507.6	507.6	507.6	507.6	506.4	360.2	360.2	360.2	360.2	356.8	296.8	268.2	236.6	236.6	236.6	236.6	236.6	233.6	233.6	233.6
22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

rurine; Lymph node Stromal cell kinase; MLSK-1; autoimmune disorder; wound healing; periodontal disease; inflammatory disease; tumour; infection; allergy; ss. Murine Lymph node Stromal cell kinase 1 coding sequence. Bird TA, Virca GD, Martin U, Anderson DM; AAC90433 standard; cDNA; 2902 BP. 26-MAY-2000; 2000WO-US014696. 99US-0136781P 19-MAR-2001 (first entry) (IMMV) IMMUNEX CORP. WO200073468-A1. 28-MAY-1999; Mus musculus. 07-DEC-2000. AAC90433; AAC90433

WPI; 2001-061546/07. P-PSDB; AAB50056 Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses.

Claim 1; Page 86-87; 106pp; English

The present sequence is the coding sequence for Murine Lymph node Stromal cell kinase 1 (MLSK-1). The protein encoded by the present sequence is useful for treating a variety of disorders listed in the disclosure of the specification, including autoimmune disorders, allergic reactions, myeloid or lymphoid cell deficiencies, wound healing and tissue repair and replacement, burns, incisions and ulcers, periodontal disease, incisions and bacterial, viral or fungal infection inflammatory diseases, tumours and bacterial, viral or fungal infection

2902 BP; 654 A; 794 C; 796 G; 658 T; 0 U; 0 Other; 100.04; Score 2902; DB 4; Length 2902; 2; Conservative 0; Mismatches 0; Indels 0; Gaps CATACTICANCACACACACACACACACACACACACACACACACACA

/*tag= a /product= "Rat SNARK protein"

Location/Qualifiers 83. .1975

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AMPK (AMP-activated protein kinase)-related kinase, designated SNARP polypeptides and polynucleotides, useful for treating or preventing diabetes, or other disorders of lipoprotein production leading to increased levels of cholesterol.

Example; Fig 2; 94pp; English

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Lefebure

Rosen CF,

Drucker DJ,

WPI; 2002-241747/29. P-PSDB; AAE19885

03-AUG-2000; 2000US-0222650P 12-MAR-2001; 2001US-0274613P. 28-MAR-2001; 2001CA-02340783.

(ONEO-) 1149336 ONTARIO INC.

02-AUG-2001; 2001WO-CA001109

WO200212456-A2

14-FEB-2002

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The invention relates to an AMPK (AMP-activated protein kinase) related kinase, designated SNARK polypeptides and polynucleotides. SNARK (SNIF/AMP-activated protein Kinase) is involved in stress response to glucose deprivation. The polynucleotides are useful for expressing SNARK protein in isolated form or as a protein conjugate. Activation of SNARK primates liver CPT-1 thus enhances lipid metabolism in liver cells and in other cell types such as heart and skeletal muscles, as well as increases GLUT-4 and glycogen in muscle. Activation of SNARK is predicted in chave insulin-like effects that would enhance the disposal of glucose into muscle and reduce plasma glucose for the treatment of diabetes and some type of disorders of lipprotein production leading to increased come type of disorders of lipprotein production leading to increased come type of disorders of triglycerides. SNARK or its variants may be administered to a subject to treat or prevent a disease associated with decreased expression of SNARK, such as disbetes. SNARK antibodies are used to modulate SNARK activity either in vivo for therapeutic purposes. SNARK antagonists may be administered to increase fuel production. SNARK antagonists may be administered to increase fuel production. Charactes of processing of the present sequence is rat SNARK CDNA suffering from hypoglycaemia. The present sequence is rat SNARK CDNA
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Pred. No. 0;
0; Mismatches 277; Indels 115; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
71.2%;
Best Local Similarity 86.4%;
Matches 2488; Conservative
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Rat; SNF1/AMPK-Related Kinase; SNARK; enzyme; stress response; diabetes; glucose deprivation; lipid metabolism; therapy; lipoprotein disorder; hyperglycaemic; drug screening; hypoglycaemia; ss.

Rattus sp

SNF1/AMPK-Related Kinase (SNARK) cDNA.

(first entry)

18-JUN-2002

AAD31710 standard; cDNA; 2929

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FTGAAGA, AAAATCA, AAAATCA, TACAACC, TCAACC		GAAACAT 	CCATGCCCCATGCCCCATGCCCCATGCCCATGCCCATGCCATGCCATGCCATGCCATGCCACCCCACCCCACCACCACCACCACCACCCCACCCCACCCC	ATCCCAI ACACCAC ACAGCAC TTGGCCC TTGGCCC	GAGCTGGA GGCTGGA GGCTGGA GGCTGGA TGCAAGG CGAAGG CGAAGG CGAAGG CGAAGG
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	TCAT TCAT TCAT CCAGC CCAGC	TTCA(ACAGC ACAGC GGCAC GGCAC GGCAC	AACCC CCACT CCACT CCACT GGGAA	
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An area of a state of a modulation of a movel indiant process.

Kinase designated 3700, and the polymuclectide sequence encoding it. The invention also describes the use of a medulator of the activity of protein kinase (PK) 3700 for making a medicament or pharmaceutical composition for modulating the ability of a cell to phosphorylate an amino acid residue of a substrate protein. Modulators of protein kinase 3700 activity are useful for modulating protein phosphorylate on a ginalling, tumourigenesis, mitogenesis, transcription of a gene, angiogenesis, tissue repair, tissue regeneration, establishment or propression of atheroselerosis, and signalling across the blood-brain barrier. The polymucleotide and polymeptide molecules for protein kinase 3700 may be used as diagnostic targets and therapeutic agents for curing pk-related disorders and cellular proliferative and/or curing pk-related disorders and cellular pholyficing, alleviating, or differentiative disorders and cellular pholyficing, and sion conting pk-related disorders and cellular pholyficing across and cellular polymucleotide sequence can be used to express protein kinase 3700 to detect a genetic alteration in a 3700 gene, in chromosome mapping, for transcrent typing, in forensic plology, and as surrogate markers. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cracricarirccicreccerrectrocrecrecrecerrecenseagreerrec 175
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                                                                                                                                                     present invention relates to the isolation of a novel human protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCGGACGGGCTCATCAAGTCGCCTAAAACCTCTGATGAAGAAGCAGGCGGTGAAGCGGC
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preventing cellular proliferative and/or differentiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3353 BP; 754 A; 1022 C; 879 G; 695 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1379; DB 6;
Pred. No. 8.2e-295;
0; Mismatches 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence encodes human protein kinase 3700
                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 47.5%;
Best Local Similarity 81.8%;
Matches 1654; Conservative
                                                                 Claim 28; Fig 1; 115pp;
                                disorders
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/*tag= a
//product= "Protein kinase 3700"
//product= "Protein kinase 3700"
//note= "The coding region (not including the terminator codon) is specifically claimed in claims 7 and 28"
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                      CACTGTCTGGATTGAGTCTCCAGTCCCTTCACACCCAAGGCTGGCCACCCTCCTCATCT
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Silos-Santiago I, Bandaru R;
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P-PSDB; ADL14161.
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Rudolph-Owen LA; Chun M, Williamson MJ; Meyers RE, Galvin KM, ξ, Hunter J New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 25643, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecules and proteins, useful for treating, e.g. cancer, heart failure and angina.

Claim 1; SEQ ID NO 43; 139pp; English.

The invention describes an isolated 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, angles, 38555 or 593 nucleic acid molecules and cany one of 40 nucleotide sequences (I). The nucleic acid molecules and cany one of 40 nucleotide sequences (I). The nucleic acid molecules and cany one of 40 nucleotide sequences (I). The nucleic acid molecules and cany one of 40 nucleotide sequences (I). The nucleic acid molecules and cany one of 40 nucleotide sequences (I). The nucleic acid molecules and can associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501, 26343, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, 26176, 26343, 56638, 18610, 33217, 21967, h1983, 26176, 26343, 56638, 18610, 33217, 21967, h1983, 26176, 26342, 26176, 26342, 26076, 2501, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26076, 26342, 26372, 26342, 26342, 26342, 26372, 26342, 26372, 26342, 26372, 26342, 26372, 26342, 26372, 26342, 26372, 26342, 26372, 26342, 26372, 26342, 26372, 26342, 26372, 26342, 26372, 26342, 26372, 26342, 263

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent din not form part of the printed specification, but was obtained in CD-ROM format directly
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K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                                                                                                       Human; full length cDNA; cDNA synthesis; oligo-capping;
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1462 TATCCCTGCTCCCAAGGAAGGCATCCTTAAGAAGTCTCGACGGGGATCTTGCTTATT 1495 1439CCTGCTCCCAAGAAGGCATCCTTAAGAAGTCCCCGAAGCGCGAGTTTGCTATT 1495 1439CCTGTCCCCAAGAAGGCACTTTGCAGAGCCCCGAAGTGTTTGTGA 1551 1436 ACTCCTCTCCCGAGCCCCGAGCCTCTCTCGACGCCCAAGTGTTTGTGA 1555 1536 GTGCGAGCCCCTGCAGCCCAAGTGATTTGTGA 1555 1536 GTGCGAGCCCCTGCAGCCCAAGCCTCTCCACCCCAAGCCTTTGACCCCCAAGCCAAGCTTTGCAAGCTCTCCCCAAGCCTCCCCCAAGCCTTCAAGCCTCCCCCAAGCTTTGCAAGCTTCCCCAAGCTTCCCCAAGCTTCCAACCTCCCCCAAGCTTTGCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCTTCCCCAAGCACCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTTGACCAACCTTCCAAGCTTTGACCAACCTTCAAGCACCACCCAC	RESULT 6 ADL30885 ID ADL30885 ID ADL30885 standard; CDNA; 3395 BP. AC ADL30885; XX C ADL30885; XX XX
382 TCAGGAAAGACAAAATCAAAGATGAGCAGGATCTGCTGCACATACGGAGGGGAGATTGAGA 14	1012 TCAACTGGGGTTACACCACCGGAGTACGGAACACCTGGTGAGGGTGGCACC

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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential theraspeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                      New oligonucleotide primers (830 cDNAs) useful for synthesizing full
length human cDNAs.
Hayashi K, Ishii S, Kawai Y;
K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                         Example 1; SEQ ID NO 2918; 1340pp; English
Ota T, Nishikawa T, Isogai T,
Wakamatsu A, Sugiyama T, Nagai
                                                                WPI; 2004-204755/20.
P-PSDB; ADL30886.
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	4.	141	136	201	184	261	244	321	304	381	364	441	424	501	484	561	544	621	604	681	664	741	724	801
SQ Sequence 3395 BP; 722 A; 1044 C; 894 G; 735 T; 0 U; 0 Other;	Query Match 47.4%; Score 1375.8; DB 12; Length 3395; Best Local Similarity 81.7%; Pred. No. 4.2e-294; Matches 1652; Conservative 0; Mismatches 337; Indels 34; Gaps	92 CIACTGCTGCCGACCCACTCCACCTCGGGGTCCCCGCACCATGGAGTCGGTTAC	77 CTACTGATTCCCTGCCGCCTTGCTCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTCG	142 TCCAGCGCCCGAGCCAGGCTCCTCGGCCTCCGCCTCGGAGAGCGCCCCGGCCCC	137 CGCGGCGCTCCGGCCCCACTCGGCCGCAGAGCTAGCCCGGCCGC	202 TGGCGGACGGGCTCATCAAGTCGCCTAAACCTCTGATGAAGAAGCAGGCGGCGCGCGC	185 TGGCGGAAGGGCTGATCAAGTCGCCCAAGCCCCTAATGAAGAAGCAGGCGGTGAAGCGGC	/ 262 ACCATCACAAACACCACGGCACCGCTACGAGTTCCTGGAGACGCTGGGCAAGGGCA	245	322 CCTACGGGAAGGTGAAGAAAGGCACGAGAGAGCTCGGGGGCGTCTGGTGGAGTCCA	305 CCTACGGGAAGGTGAAGAAGGCGCGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAA	382 TCAGGAAAGACAAAATCAAAGATGAGCAGGATCTGCTGCACATÁCGGAGGGGAGATTGAGA	365 TCCGGAAGGACAAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAG	442 TCATGTCTTCACTCAACCCCCCACATCATTGCCATCCATGAAGTGTTTGAGAATAGCA	425	502 GCAAGATTGTGATGGAGTATGCCGAGGCGAGGGGATCTGTATGATTACATCGGTG	485	562	545 AGCGGCAGCTCAGTGAGCGGAAGCTAGGCATTTCTTCCGGCAGATCGTCTGCCG	622 IGCACTACTGCCACCAGGAACGGGATCGTTCACCGAGATCTCAAGCTGGAAACATCCTTC	605	682 TAGATGCCAATGGAACATCAAGATTGCTGACTTTGGCCTCTCCAACCTGTACCACAAAG	665 TGGATGCCAATGGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAG	742 GCAAGTICCTCCAGACGTICTGGGGAGCCCTCTCTACGCCTCGCCT
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ò	CCCTATGTGGGCCCAGAGGTGGACAGCTGGTCTCTGGGCGTTCTCCTGTACAT	61
Db	SCCCTACACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATC	44
Š	ATGGCACCATGCCCTTTGACGGGCAGGATCATAAAACACTGGTGAAGCAAAT	
qq	845 TGGTGCATGGCACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCA 9	4
ò	922 GTAACGGGGCTTACCGTGAGCCGCCAAGCCGTCCGATGCCTGTGGCCTGATCCGGTGGC 9	81
qq	CAACGGGGCTACCGGGAGCCACTAAACCCTCTGATGCCTGTGGCCTGATCGGTGG	64
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, è	82 TGCCTCPABABTCTCTCABAGGTGAGGTGAGGAATACCTCTTTTCCCTCGAGGAAGAA 1	, 4
7 E	65 TIGGCCCAGTCCAACGCCCCAACGATGACACCCCAACGACCAACGACCAACGACCAACGCCCAACGACCAACAA	124
ìè	42 GCCTTTABAGCTATATCTTABAGABABABATCTTTTTTTTTT	; ⊂
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δλ	762 CAGGGGCTGTGAGTGAGGACAGCATCCTGTCCTCCGAGTCCTTTGACCAATTGGACTTGC 1	821
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oy B	1822 CTGAACGTCTTCCCGAAACCCCACTGAGGGCTGTGTGTCTGTGGACAACCTGAGGGGGC 1/	881 855

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                                                                                                            2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity and to down regulate. This man activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence encodes a polypeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
                TIGAGGAGCCCCCCTCAGAGGCCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTT
                                                                                  CCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAAAGGAATGGTGCCCTAGTATGGGGTAG
 GTCTGAAGCGATGGTGGCAGGAATCCT
                                                               TGGGGGACAGCTGCTTTTCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGG
                                          TGGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGCCTACAGACAAG
                                                                                                          CACTGAGGGTCTGCTCAAAGCTCACCTGAGTGGAGTAGGCATTGCCCCAG-CCCGGTCAG
                                                                                                                                                                                                                                                                                                Human; gene; gene therapy; vaccine; disease treatment; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3443;
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                                                                                                                                                                                                                                                                           Human cell cycle-associated cDNA from clone DKFZphtes3_7j3
                                                                                                                                2092
                                                                                                                                              Score 1374.2; DB 5; Length
Pred. No. 9.5e-294;
0; Mismatches 338; Indels
                                                                                                                               GCTCTGAGAGGGTTTGCAGAGGAACCCTGGGTCGGATTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 942-943; 1095pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEHU-) GERMAN HUMAN GENOME PROJECT.
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ilarity 81.6%;
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Best Local Similarity
Matches 1651; Conserv
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                                      TGGCTCAAAATCTGCAAGGTGACCCGGCTGAGGATACCTCTTCTCGCCCTGGCAAGAGCA
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GCACTGTACCTGGGCTGGAGCGCCAACATTCTCTTAAGAAGTCCCGAAAGGAGAATGACA
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Claim 2; SEQ ID NO 639; 918pp; English.

Novel human secreted and transmembrane protein cDNA SeqID 639. human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; ADF76964 standard; cDNA; 3443 BP (first entry) 26-FEB-2004 ADF76964; RESULT 8
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ss; gene ö polypeptides, useful for diagnosing and treating an immune disorder, e.g. systemic lupus erythematosus, rheumatoid is, osteoarthritis, juvenile chronic arthritis, thyroiditis mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour; Schoenfeld JR; Jackman JK, Hunte B, , Wu TD; 22-FEB-2002; 2002US-0359461P. 21-FEB-2003; 2003WO-US005241 Clark H, F, Wood WI, (GETH) GENENTECH INC WPI; 2003-721702/68 diabetes mellitus. P-PSDB; ADF76965 WO2003072035-A2. / SC, Homo sapiens. 04-SEP-2003 arthritis, Williams New PRO related Bodary

This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular corganisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information, crecived from orber cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, curropeptides and hormones) which are received and interpreted by diverse cell receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a timulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating edetecting the expression of a tumour associated gene. The present nvention.

141 146 201 194 261 254 321 314 87 chachdannecerececennecheacerechechecendadenechechechechechechen 255 ACCACCACAAGCACAACCTGCGCACCGCTACGAGTTCCTGGAGACCCTGGGCAAAGGCA 82 CTACTGCTGCCCGACCCACTCCACCTCGCGGTCCCCCGCACCATGGAGTCGGTGGCCTTAC 147 CGCGGCGCTCCCGCCCACTCCCTCGGCCGCGAGAGCTA-------GCCCGGCCGC 202 TGGCGGACGGGCTCATCAAGTCGCCTAAACCTCTGATGAAGAAGCAGGCGGTGAAGCGGC ACCATCACAAACACAACCTGCGGCACCGCTACGAGTTCCTGGAGACGCTGGGCCAAGGGCA 142 TCCAGCGCCCGAGCCAGGCTCCCTCGGCCTCCGCCTCGGCCTCGGAGAGCGCCCGGCCGC 195 TGGCGGAAGGGTGATCAAGTCGCCCAAGCCCCTAATGAAGAAGCAGGCGGTGAAGCGGC 34; Gaps Score 1374.2; DB 10; Length 3443; Pred. No. 9.5e-294; 0; Mismatches 338; Indels 34; (Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other; Query Match
Best Local Similarity 81.6%;
Matches 1651; Conservative Query Match Best Local Similarity 262 엄 ò g ò g ò 셤

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322 CCTACGGGAAGGTGAAGGACGCCGGGCGTCTTGGTGGCCATCAAGTCCA 391 315 CCTACGGGAAGGTGAAGAAGCCCGGGAGGCCTGGTGGCCATCAAGTCAA 374 316 CCTACGGAAAGGTGAAGAAGCCCGGGAGGCGTCGTGGCCATCAAGTCAA 374 317 TCAGGAAAGACAAAATCAAAGAAGCTCGGGGCGTGATGAGGAATTGAA 411 318 TCAGGAAAGACAAAATCAAAGAAGACAAATTGCCAATACGGAGGGGAGTATTGAA 411 319 TCAGGAAAGACAAAATCAAAGACAAAATTGCCAATACGGAGGGAG		1162 TCCTGGAGATGGAGCCAAGGTGGAGCAGGAGGTGGAA 1221

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PA (SCHO/) SCHOCH C.

PA (KERN/) KERN W.

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PI Haferlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;

PI Ells R, Brors B, Mergenthaler S;

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WPI; 2003-505037/47.

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PT Determining the subtype of leukemia cells and whether a patient sample contains leukemia cells or other cells, useful for treating leukemia, PT comprises determining the expression profile of a group of markers in a patient sample.

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PT Determining the subtype of leukemia cells and whether a group of markers in a patient sample.

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CC The present invention relates to a method (MI) for determining the subtype of leukaemia cells and whether a patient sample contains

CC The present invention relates to a method (MI) for determining the subtype of leukaemia cells and whether a patient sample contains

CC The present invention relates to a method is useful for determining the presence of leukaemia cells, its types or subtypes, and contains the preparation of a medicament for treating leukaemia.

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CC determining the presence of leukaemia cells, its types or subtypes, and for the preparation of a medicament for treating leukaemia.
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4; CCCGGCCCCCCACTCCCTCGGCCGCAGAGCTA-------GCCCGGCCGC 194 CTACTGCTGCCCGACCCACTCCACTCGCGGTCCCCGCACCATGGAGTCGGTGGCCTTAC 141 cracidarnececrecerrecrerecrecrecerrecresearcecreerrecriserrance 146 201 254 ACCATCACAAACACAACACTGCGGCACCGCTACGAGTTCCTGGAGACGCTGGGCAAGGGCA 321 ACCACCACACACACACCTGCGGCACCGCTACGAGTTCCTGGAGACCCTGGGCAAAGGCA 314 TCAGGAAAGACAAAATCAAAGATGAGCAGGATCTGCTGCACATACGGAGGAGATTGAGA 441 501 621 614 674 TGGCGGACGGCTCATCAAGTCGCCTAAACCTCTGATGAAGAAGCAGGCGGTGAAGCGGC 261 CCTACGGGAAGGTGAAGAAGGCACGAGAGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCA 381 CCTACGGGAAGGTGAAGAAGGCGCGGAGAGCTCGGGGCCCTGGTGGCCATCAAGTCAA 374 GCAAGATTGTGATTGTCATGGAGTATGCCAGCCGAGGCGATCTGTATGATTACATCAGTG 561 TGCACTACTGCCACCAGAACGGGATCGTTCACCGAGATCTCCAAGCTGGAAAACATCCTTC 681 TCCAGCGCCCGAGCCCCCTCGGCCTCCGCCCTGGCCTCGGAGCGCCCCGGCCGC **AGCGGCCACGGCTGAGTGAGCGGGACGCCAGGCATTTCTTCCGACAGATCGTGTCTGCCC** TGCACTATTGCCATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCT Gaps Query Match
47.4%; Score 1374.2; DB 10; Length 3443;
Best Local Similarity 81.6%; Pred. No. 9.5e-294;
Matches 1651; Conservative 0; Mismatches 338; Indels 34; C Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other; Query Match Best Local Similarity 82 87 142 147 202 255 315 375 442 502 555 622 195 262 322 382 435 495 562 615 682

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වූ	855 T	SCATGGCACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCA 91
δ	922 G	STGGCCTGATCCGGTGGC 98
Ор	915 G	GGGGCCTACCGGGAGCCACCTAAACCCTCTGTGTGTGTGT
λ̈	982 T	GITAATGGTGAACCCCACCCGTCGGGCCACACTGGAGGATGTAGCCAGTCATTGGTGGG 10
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٥٨	1042 T	CAACTGGGGTTACACCACCGGAGTCGGGGAACAGGAAGCCCTGCGTGAGGGTGGGCACC 11
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ò	1222 G	CTCTTAAGAAGTCCCGAAAGGAGAATGACA 12
Ob	1215 G	CCACCCCTGGCCTGGAGCGCCAGCATTCGCTCAAGAAGTCCCGCAAGGAGAATGACA 127
δ	1282 T	GGCTCAAAATCTGCAAGGTGACCGGCTGAGGATACCTCTTCTCGCCCTGGCAAGAGCA 13.
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Db	1626 G	CATCCTCAAACTCAATGGCAAGTTCTCCCAGACGTCTTGGAGCTCGCGGCCCCCACCA 168
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central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polynucleotide
                                                                                                                                                                                                                                                                                        DB 12; Length 3443;
                                                                                                                                                                                                           Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                    Query Match
47.4%; Score 1374.2; DB 12; Lengt
Best Local Similarity 81.6%; Pred. No. 9.5e-294;
Matches 1651; Conservative 0; Mismatches 338; Indels
                                                                                                                               the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic arthritis, softemis systemic haemolytic anomia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the
                                                                                                                                                                                                                                                                                        TGGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGCCTACAGACAAG
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This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to buman tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polynucleotide sequence is a human kinase DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              v nucleic acid molecule encoding a kinase polypeptide, useful for
sparing a composition for treating diseases or disorders, e.g., cancer,
neurological, immunological or inflammatory disorders.
                                                                                                                                          gene; ds; kinase; human; SNP; single nucleotide polymorphism; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease; cardiavascular disease; brain; neuronal associated disease; metabolic; inflammatory disorder; cytostatic; neuroprotective; immunomodulator; antinflammatory disorder; calcium/calmodulin-dependent protein kinase; NuaK2.
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                                                                                                                                                                                                                                                                                                                          New isolated arginine-rich protein-like polynucleotides and polypeptides, useful for diagnosing and/or treating conditions associated with aberrant activity of the arginine-rich polypeptides, such as cancer and
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                                                                                                                                              05-MAR-2001; 2001US-00799451.
05-MAR-2002; 2002WO-US005095.
20-AUG-2002; 2002US-00225251.
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(XUEA/) XUE A.
(DRMA/) DRMANAC R T.
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                  GCATTCTCAAACTCAATGGCAAGTTCTCCCGCACAGCCTTAGAAGGCACTACCCCTAGCA
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Ghosh M;
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Yamazaki V, Chen R, Wang Z,
J D, Drmanac RT;
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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature procein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The cocoded polypeptides (ABR68902-ABR68949) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cellinaging, screening and diagnostic assays and for treating cellinaging, screening and disorders, neurodegenerative diseases (Parkinson's or Alzheimer's disease), autonimme diseases (multiple sclerosis, diabetes, lupus) genetic disorders, wound, burns, incision, ulcers, liver or lung fibzonsis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format contractly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as
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                                          CTGAACGCTCCCAGAGCCCCCACTGCGGGGCTGTGTGTTTTGTGTGTAACGCTCAACCTCACGGGGC
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                                                                                                                                                                                                                                                                                             TGGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGCCTACAGACAAG
                                                                                                                                                                                                                                                                                                                                            ----GTCTGAAGCGATGGTGGCAGGAATCCT
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/product= "Human PKIN-12 protein"
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                                                                                                                                           TTGAGCAGCCTCCCTCAGAAG
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23-JUN-2000; 2000US-0213467P.
30-JUN-2000; 2000US-0215651P.
07-JUL-2000; 2000US-0216605P.
13-JUL-2000; 2000US-0218050P.
25-AUG-2000; 2000US-0218056P.
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The invention relates to human kinase PKIN proteins and their

Corresponding cDNAs. A composition containing PKIN agonist is useful for

Creating a disease or condition associated with decreased expression of

PKIN and a composition comprising PKIN antagonist is useful for treating

a disease or condition associated with overexpression of PKIN. The

disease or condition associated with overexpression of PKIN. The

disease or condition associated with overexpression of PKIN. The

disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,

myeloma, sarcoma, teratocarcinoma, Hoddison's disease,

CC disorder Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,

CC autoimmune thyroiditis, gout, bronchitis, Cron's disease, disease,

CC autoimmune thyroiditis, gout, bronchitis, psoriasis, Reiter's syndrome,

CC autoimmune thyroiditis, gout, bronchitis, psoriasis, Reiter's syndrome,

CC autoimmune thyroiditis, syndrome, uveitis, ulcerative colitis,

CC allitis, multiple sclerosis, syndrome, uveitis, ulcerative colitis,

CC rheumatoid arthritis, Siogran's syndrome, uveitis, ulcerative colitis,

CC creating's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio

CC vascular disease (arteriovelers) cirrhosis, hepatitis,

CC vascular disease (arteriovelers) and cumours); lipid

disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,

CC pkin-12 cDNA comprise human kinase polypeptides Page 184; 197pp; English Claim 5;

Sequence 3360 BP; 729 A; 1022 C; 882 G; 727 T; 0 U; 0 Other;

145 205 265 385 445 505 621 201 261 321 381 CCTACGGGAAGGTGAAGAAGGCGCGGGAGGCTCGGGCGCCCTGGTGGCCATCAAGTCAA 325 441 501 561 681 TGCACTATTGCCATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCT 625 98 TGGCGGAAGGGCTGATCAAGTCGCCCAAGCCCCTAATGAAGAAGCAGGCGGTGAAGCGGC TCATGTCATCGCTCAACCACCCTCACATGATGTTTTGAGAACAGCA GCAAGATCGTGATCGTATGGAGTATGCCAGCCGGGCGACCTTTATGACTACATCAGCG AGCGGCCACGGCTGAGTGGCGGGACGCCAGGCATTTCTTCCGACAGATCGTGTCTGCCC CTACTGCTGCCCGACCCACTCCACCTCGCGGTCCCCGCACCATGGAGTCGGTGGCCTTAC cecedececrecescecearecereses. CCTACGGGAAGGTGAAGAAGGCACGAGAGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCA TCAGGAAAGACAAAATCAAAGATGAGCAGGATCTGCTGCACATACGGAGGAGATTGAGA GCAAGATTGTGATTGTCATGGAGTATGCCAGCCGAGGCGATCTGTATGATTACATCAGTG TGCACTACTGCCACCACACGCGATCGTTCACCGAGATCTCAAGCTGGAAAACATCCTTC TCCAGCGCCCGAGGCCAGGCTCCCTCGGCCTCGGCCTCGGAGAGAGCGCCCGGCCGC TGGCGGACGGGCTCATCAAGTCGCCTAAACCTCTGATGAAGAAGCAGGCGGTGAAGCGGC ACCATCACAAACACACCTGCGGCACCGCTACGAGTTCCTGGAGACGCTGGGCAAGGGCA Accedenceacteacteacteactaactaaccaritrerreceacaarcererece Gaps Length 3360; 35; 47.2%; Score 1370.6; DB 6; Length llarity 81.5%; Pred. No. 5.9e-293; Conservative 0; Mismatches 339; Indels Query Match Best Local Similarity Matches 1649; Conserv 39 142 66 146 909 82 202 262 506 322 266 382 326 442 386 502 446 562 622 999 g g g g 8 g 요 g ò g ò 8 à ò ò ઠે 8

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1105 1516 1161 1221 1401 1641 1701 1101 GCACTGTACCTGGGCCGGAGCGCAACATTCTCTTAAGAAGTCCCGAAAGGAGAATGACA 1281 TGGCCCAGTCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCA 1285 1581 TGTTAATGGTGAACCCCACCCGTCGGGCCACTGGAGGATGTAGCCAGTCATTGGTGGG 1041 AGGAGGACCCTCAGGAACTCAGACCGGTGCCTGATACTCCAGGGCAGCCTGTCCCTGCTG 1461 745 925 985 801 861 921 régrécargecaccarecerricargeceargaccaradagarceragiqua 865 981 1106 TCCTGGAGAATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAA CTGGCAGTGACTCTGCCCGCGCCTCCATGGCTGACTGGCTCCGGGGGTTCCTCCCGCCCCC GCCTTAAGCTTCCGAAAGGCATTCTCAAGAAAAAGTCCTCTACCTCGTCAGGGGAGGTAC 1286 ACCTCAAGCTGCCAAAGGGCATTCTCAAGAAGAAGGTGTCAGCCTCTGCAGAAGGGGTAC ACTCCTCTCCCGAGCCCAGTGAATCTGGGGAGCTCTTGGACGCAGGCGACGTGTTTGTGA GCATTCTCAAACTCAATGGCAAGTTCTCCCGCACAGCCTTAGAAGGCACTACCCCTAGCA TAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCTCTCCAACCTGTACCACAAAG TGGGTGCCAATGGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAG GCAAGTTCCTCCAGACGTTCTGTGGGAGCCCTCTCTACGCCTCGCCTGAGATAGTCAACG 686 GCAAGTTCCTGCAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATG GGAAGCCCTATGTGGGCCCCAGAGGTGGACAGCTGGTCTCTGGGCGTTCTCCTGTACATCC GGAAGCCCTACACAGGCCCAGAGGTGGACAGCTGGTCCTGGGTGTTCTCCTCTACATCC TGGTGCATGGCACCATGCCCTTTGACGGGCAGGATCATAAAAACACTGGTGAAGCAAATCA TCAACTGGGGTTACACCCACCGGAGTCGGGGAACAGGAAGCCCTGCGTGAGGGTGGGGCACC CTAGTGGTGACTTTGGCCGGGCCTCCATGGCGGACTGGTTACGTCGCTCCTCGCGCCCCCC TCCTGGAGAATGGAGCCAAGGTGTGCAGCTTCTTCAAGCAGCACGTGCCGGGAGGTGGAA TGGCTCAAAATCTGCAAGGTGACCCGGCTGAGGATACCTCTTCTCGCCCTGGCAAGAGCA 1462 TATCCCTGCTCCCAAGGAAAGGCATCCTTAAGAAGTCTCGACAGCGTGAATCTGGTTACT ACTCCTCTCCAGAGCCCCAGCGAGTCTGGGGGAACTCTTAGACGCCAGTGATGTTTGTGA GTGGGGACCCCGTGGAGCAGAAGTCTCCACAGGCTTCAGGGCTCCTCCTCCACCGCAAGG CCTTTGGCTCCCTGGACCAACTGGCCTCCTCCATCCTGCAGCCCGGCCCAGCCGCCCT GTAACGGGGCTTACCGTGAGCCGCCCAAGCCGTCCGATGCCTGTGGCCTGATCCGGTGGC 1642 (626 742 802 746 908 998 1042 1102 1046 1162 1222 1282 1226 1342 1400 1522 1457 1582 682 862 922 982 926 986 1702 1402 · & g ò 유 à g ò g 8 원 8 원 ò 셤 ò a 8 a ò 유 ò a ò 셤 ò 셤 ò 임 ò 셤 ò 셤 à

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cytostatic; cardiant; hypotensive; antianginal; osteopathic; antirheumatic; neuroprotective; antinflammatory; antipsoriatic; antirheumatic; neuroprotective; antinflammatory; anglogenesis inhibitor; antiadovascular; virucide; analgesic; was anglogenesis inhibitor; antidopatedis simulator; cerebroprotective; perprotective; nephrotropic; antithyroid; dermatological; immunomodulator; cell discretion disorder; parain disorder; platelet disorder; colon disorder; was brain disorder; renal disorder; breast disorder; colon disorder; kinney disorder; recevical disorder; spleen disorder; thymus disorder; phonorated disorder; pancreatic disorder; testes disorder; haematopoietic disorder; phonorated disorder; mascle disorder; skeletal muscle disorder; skin disorder; metabolism disorder; immune disorder; metabolism disorder; immune disorder; metabolic disorder; liver disorder; interpretation disorder; metabolic disorder; neurological disorder; viral disease; pain disorder; metabolic disorder; neurological disorder; cancer; heart failure; blood vessel disorder; anglogenic disorder; cancer; heart failure; hyperical anglogenic disorder; cancer; heart failure; hyperical anglogenic disorder; cancer; heart failure; hyperical disorder; anglogenic disorder; heart failure; hyperical disorder; anglogenic disorder; cancer; heart failure; hyperical disorder; heart failure; hyperical disorder; should disorder; heart failure; hyperical di
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                                                              1697 CAGGGCTGTGAGCGAGGACAGCATCCTGTCCTCTGAGCTTTGACCAGCTGGACTTGC
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CAGGGCTGTGAGTGAGGACAGCATCCTGTCCTCCGAGTCCTTTGACCAATTGGACTTGC
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cell proliferation; cell differentiation; cell growth; cell division;
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New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecules and proteins, useful for treating, e.g. cancer, heart failure and angina.
                                                                                                                                                                                                                                                            Rudolph-Owen LA;
Chun M, Williamson MJ;
                                                                                                                                                                                                                                                            Hunter JJ, Meyers RE,
, Tsai F, Galvin KM,
                                                                           2000US-0257511P.
2001US-0260166P.
2001US-00797039.
                                                                                                                                                                                                                                                                           Silos-Santiago I, Bandaru R;
                                                                                                          2001US-00909743
2001US-00920346
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2001US-0312539P
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                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                   Olandt PJ,
                                                                                                                                                                                                                                                             Kapeller-Libermann R,
                                                                                                                                                                                                                                                                                           WPI; 2004-268788/25.
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                             25-SEP-2000;
25-SEP-2000;
                                                             14-NOV-2000;
                                                                     L5-NOV-2000;
                                                                                   05-JAN-2001;
28-FEB-2001;
                                                                                                   27-APR-2001;
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25-SEP-2001;
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                                                                                                                                                                                                                                                                    Curtie RAJ.
                                                                                                                                                                                                      2-AUG-2002
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The invention describes an isolated 21910, 56634, 55053, 2504, 15977, CC 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, CC 21967, h1983, m1983, 33655 or 593 nucleic acid molecule (I) comprising any one of 40 nucleotide sequences (I). The nucleic acid molecules and polypeptides are useful for diagnosing and treating a subject having a disorder, which is a sesociated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501, CC 37003, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, CC differentiative disorders, kidney (renal) disorders, breast cdisorders, prostate disorders, cervical disorders, spleen covarian disorders, prostate disorders, testes disorders, chematopoietic disorders, pancreatic disorders, relate an uscle disorders, inflammatory disorders, cardiovascular disorders, conducted disorders, disorders, disorders, disorders, disorders, disorders, and disorders, cardiovascular disorders, conducted disorders, netabolic disorders, netabolic disorders, blood vessel disorders or angiogenic disorders, experimential calmed, e.g. cancer, heart failure, hypertension, candina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease, psoriasis, or asthma. The nucleic acid molecules and colloses, erg. cell larger encodes a novel human protein of the invention. Colvision. This sequence encodes a novel human protein of the invention. Note: The sequences given in the specification are also avaialable in

990S-00365162. 990S-00392189. 990S-00412210. 99US-00448076. 2000US-0186061P.

09-SEP-1999; 05-OCT-1999; 23-NOV-1999; 29-FEB-2000;

98US-00163821. 99US-0117580P. 99US-00276400.

27-JAN-1999 25-MAR-1999 30-SEP-1998

25-APR-2003; 2003US-00423543

25-MAR-2004

Claim 1; SEQ ID NO 45; 139pp; English.

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                                                                                                            GCTACGAGTTCCTGGAGACGCTGGGCAAGGGACCTACGGGAAGGTGAAGAAGGCACGAG 348
                                                                                                                                                                AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACA 468
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                                                               CCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAGCTCAGTGAGCGCAAG
                                                         CCTCCGCCCTGGGCTCGGAGAGCGCCCGGCCGCTGGCGACGGGCTCATCAAGTCGCCTA
                                                                                  AACCTCTGATGAAGAAGCAGGCGGTGAAGCGGCACCATCACAAACACAACCTGCGGCACC
                                                                                                                                                                                                                   AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGC
                                             Gaps
                                12; Length 1884;
                                             21;
                   Sequence 1884 BP; 403 A; 599 C; 548 G; 334 T; 0 U; 0 Other;
                               Query Match
46.9%; Score 1360.2; DB 12; Length
Best Local Similarity 84.2%; Pred. No. 9.9e-291;
Matches 1565; Conservative 0; Mismatches 273; Indels
      ftp.seqdata.uspto.gov/sequence.html?DocID=20040058355
format
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 ACTGCCAAGAGGTGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC
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 ACTGCCAGGAGGTGACAGCGACAAGCCATACCGAGGGTCTGCTCAAAGCTCACC
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 ATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATCTGCAAGGTGACCCGG CCCAGACAGCTTAGAGCTCGCGGCCCCCACCATCGGCTCCCTGGATGAACTCGCCC TGGCTGACTGGCCTCCGGCGTTCCTCCCGCCCCTCCTGGAGAATGGGGCCAAGGTGTGCA GCTTCTTCAAGCACGTGCCGGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGGCAAC GCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACCCCTGGCCTGGAGCGCCAGC CTGAGGATACCTCTTCTCGCCCTGGCAAGAGCATCTTAAGCTTCCGAAAGGCATTCTCA TGGCGGACTGGTTACGTCGCTCCTCGCGCCCCCTCCTGGAGAATGGAGCCAAGGTGTGCA 1766 1129 995 1189 1055 1249 1115 1309 1175 1369 1235 1429 1295 1609 1466 1669 1729 1789 1646 1849 1706 1903

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SUMMARIES	ID	AK004737	AK033672	AK034082	AY399041	AY399039	AY399040	BI653092	CA319312	CF72923	BG915967	CF726196	CB248251	CO424322	C0041415	CF584809	BI143828	C0041178	BF785290	BB625283	CK781308	BG174288	BG694881	BF789245	BI143493
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25	56	27	28	29	30	31	c 32	33	34	35	36	37	38	39	40	41	42	43	44	45

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ALIGNMENTS

AKO04737 Mus musculus adult male lung CDNA, RIKEN full-length enriched library, clone:1200013B22 product:weakly similar to PROBABLE SERINE/THEREONINE-PROTEIN KINASE KIAA0537 (BC 2.7.1) [Homo sapiens], full insert sequence. AKO04737. GI:26334437 AKO04737. AKONO,H., Okazaki,Y., Hayatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes CO0493344	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Nakamura, S., Hazada, A., Nishima, T., Makamura, S., Hazada, A., Yamamoro, R., Matsumoto, H., Sakguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tranka, T., Matsunra, S., Kawai, J., Yoneda, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 2053091310768614 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection buture 409, 685-690 (2001)
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CGAGCCCAGGCTCCCTCGGCCTCCGCCCTGGCCTCGGAGAGCGCCCCGGCCGCTGGCGGACG
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                                                                                                                                                  Length 2899;
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                                                                                                                                             Score 2865.8;
Pred. No. 0;
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                             /note="putative"
2899
/note="putative"
                                                                                                                                           98.8%;
Best Local Similarity 99.9%;
Matches 2867; Conservative
         .2881
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences or Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, On Dec 10, 2002 this sequence version replaced gi:12836134. Please visit our web site (http://genome.gsc.riken.jp/) for further
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PRKGTLKKSRQRESGYYSSPEPSESGELLDASDVFVSGDPVEQKSPQASGLLLHRKGT
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PERLOEKFSRTALEGTTPSTFGSLDQLASSHPAARPSRPSGAVSEDS ILSSESFPQLDL
GICSKLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="unnamed protein product; putative weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-) [Homo sapiens] (SWISSPROT|060285, eridence: FASTY, 56.8% ID, 98.6% Length, match=1849)"
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SMADWLRRSSRPLLENGAKVCSFFKQHVPGGGSTVPGLERQHSLKKSRKENDMAQNLQ
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full length cDNAs
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                                                                                                                                    Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Inchani, Y., Itch, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Itch, M., Izawa, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshina, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshina, Submission
  FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                        Nature 420, 563-573 (2002)
6 (bases 1 to 2899)
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LKLNGKFSRTALEGTTPSTFGSLDQLASSHPAARPSRPSGAVSEDSILSSESFDQLDU
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                                                                                                                                                                                    /note="unnamed protein product; putative weakly similar to PROBABLE SERINE/THERONINE-PROTEIN KIN KIAA0537 (EC 2.7.1.-) [Homo sapiens] (SWISSPROT|060285, evidence: PASTY, 56.0%ID, 98.6%length, match=1849)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ibhii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Ibhii,Y., Nakamura,S., Hazama,M., Nishine,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watchif,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Oxawa,X., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Rangqawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL.http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Labbratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/strain="C57BL/63"
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/db_xref="taxon:10090"
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1711 CCCTGGACCAACTGGCCTCCTCCAGCGCCCGGCCCCACCGCCCCTCAGGGGCCTG 1770	1741 TGAGTGAGGACAGCATCCTGCTCCTCTGACCAATTGGACTTGCCTGAAGGTC 1800	TTCCCGAAACCCCACTGAGGGCTGTGTCTGTGTAGAACCTGAGGGGCTTGAGCAGC 186	CICCITAGARGEICIGARGEGAIGEIGEGAGGAAICCIIGGGGGGGIACIGCIIIIIIIIII	1951 TGACAGACTGCCAAGAGGTGACTGCAGCCTACAGACAGCCCTAGGAATCTGCTCAAAGC 2010 	2011 TCAGCTGAGGAAGGGAGATGGTGCCCTAGTATGGGGTAGGCTCTGAGAGGGTTTGCAGAG 2070 	2071 GAACCTGGGTTCGTCTCCAGTGAATAGAGTACATCAAGGGCTCTACGTCTGCAGCC 2130	2131 TGACTGAACCTGAAGATGAGAGATCGCATTGATGTGGAAAGGAATGGGAACCCTTGC 2190 	2191 TGCCCGAGTGTTATAGTGGGGTGGCCTGAAGGTGCCTACCTCCTTTGTGCCATGAGTGTC 2250	ACCCATGACATTCCCACCCTGTTCTCGGCTGCACCTTCACATAAGTTTCTGTTTCCAT 	2311 CAACCACCAGGGTTAGAACCCTGAGTGCGAGGTAATGTGTAGTGACTGCCATTATT 2370 2281 CAACCACCAGGGTTAGAACCCTGAGTACTGCGGAGGTAATGTGTAGTAGTGACTGCCATTATT 2340	2371 TAGAGAGAAACAGCCTCTGGTTTCCATCTCTGCTGCTGTGCATCTCAAAGACCTGGGAA 2430 	2431 GACTCGGACCGCTGTTTGACTTCATCTCAAGGGGACCAGATGCCCCTGGACCCCATCTTA 2490 2401 GACTCGGACCGCTGTTTGACTTCATCTCAAGGGGACCAGATGCCCCTGGACCCCATCTTA 2460		2551 TTTCTCAGGCCAACGGGACCTAGAATGTGCTGACTTATTTTTTTT	2611 TCTGTTTTTGGTTTTTGTTTGTTTGTTTTTGTTTTTAGGAATTTTGCTGTT 2670 	2671 CAATAAIGIGAAIGCIGIGITCIGGGGAACTCCACIGIGCCACIGAAGITTAIGIACAGA 2730 	2731 GAAGTATTTGGCAATGATGTCCCTCTATTCAAGGGGGGTGGGGGCGTTTTTCAAATGTAT 2790 	2791 GTCTTGAGCACTGTCTGGATTGAGTCTCCAGTCCCTTCACACCCAAGGCTGGCCACCCTC 2850
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31 GCCACCAGAACGGATCGTTCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCA 	691 AIGGAAACATCAAGATTGCTGACTTTGGCCTCTCCAACTGTACCACAAAGGCAAGTTCC 750	751 TCCAGACGTTCTGTGGGAGCCCTCTCTACGCCTGGCTGAGATAGTCAACGGGAAGCCCT 810	811 ATGTGGGCCCAGAGGTGGACAGCTGGTCTTGGGCGTTCTCCTGTACATCCTGGTGCATG 870	871 GCACCATGCCCTTTGACGGCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGG 930	931 CTTACCGTGAGCCGCCAAGCCGTCCGATGCCTGTGGCCTGATCCGGTGGCTGTTAATGG 990	991 TGAACCCCACCCGTCGGGCCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAACTGGG 1050	GTTACACCACCGGAGTCGGGAACAGGAAGCCCTGCGTGAGGGTGGGGCACCTTAGTGGTG	ACTITIGACCGGGCCTCCATGGCGGACTGGTTACGTCGCTCCTCGCGCCCCTCCTGGAGA	arggagccaaggrgrgcagctrctrcaagcagcagcaggaggggggaaggaagcacrgracargcaaggaagg	1231 CTGGGCTGGAGGGGGACATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAA	ATCTGCAAGGTGACCCGGCTGACGTCTTCTCGCCCTGGCAAGAGCAGCTTAAGC 	1351 TTCCGAAAGGCATTCTCAAGAAAAGTCCTCTACCTCGTCAGGGGAGGTACAGGAGGCC 1410	1411 CTCAGGAACTCAGACCGGTGCCTGATACTCCAGGGCAGCCTGTCCCTGCTGTATCCCTGC 1470	71 TCCCAAGGAAAGGCATCCTTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCTCTCT	CAGAGCCCAGCAGATCTGGGGAACTCTTAGACGCCAGTGATGTGTTTGTGAGTGGGGACC	91 CCGTGGA	51 AACTCAATGGCAAGTTCTCCCGCACACGCTTAGAAGGCACTACCCCTAGCACCTTTGGCT	1621 AACTCAATGGCAAGTTCTCCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCT 1680

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Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.jp,
URL:http://genome.gec.riken.jp, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="unnamed protein product; putative weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-) [Homo sapiens] (SWISSPROT|060285,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'protein id="BAC28575.1"
'db_xref="GI:26329673"
'translation="MESGALLQRPSQAPSASALASESARPLADGLIKSPKPLMKKQAV
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REIEIMSSLNHPHIIAIHEVGRSRLVTVFENSSKIVIVMEYASRGDLYDYISERPRLS
ERDARHFFRQIVSALHYCHQNGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFL
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LLLHRKGIILKLNGKFSRTALEGTTPSTFGSLDQLASSHPAARPSRPSGAVSEDSILSS
ESFDQLDLPPRLPETPLRGCVSVDNIRGLEQPPSEGIKRWWQESLGDSCFSLTDCQEV
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PSGDFGRASMADWLRRSSRPLLENGAKVCSFFKQHVPGGGSTVPGLERQHSLKKSRKE
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                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                          prepare mouse Lissues.
Please visit our web site for further details.
URL:http://gonome.goc.riken.jp/
URL:http://fantom.goc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FANTOM_DB:9330154N24"
/db_xref="taxon:10090"
/clone="9330154N24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
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98. .2017
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AK034082

2869 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male diencephalon cDNA, RIKEN FULL-length
enriched library, clone:9330154N24 product:weakly similar to
PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2869)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                  High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                           Mus musculus HCM0091 gene, VIRTUAL TRANSCRIPT, partial sequence, AY399041
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                              TITITAAGTGAATITIGCTGCTTTCAATAATGTGAATGCTGTGTTCTTGGGGGAACTCCACT
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gene trios Science 302 (5652), 1960-1963 (2003) 14671302 2 (Bases 1 to 1887) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Bockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment. Location/Qualifiers 1. 1887 //organism="Homo sappens" // Organism="Homo sappens" // Organism="Homo sappens" // Ab_xref="taxon:9606" // Ibous_tag="HCM0091"	tch al Similarity 78.5%; Score 1264; DB 9; Length 1887; al Similarity 78.5%; Pred. No. 7.1e-287; 1461; Conservative 0; Mismatches 380; Indels 21; Gaps 2; 169 CCTCCGCCCTGGCCTGGAGAGCGCCCGGCCGGAGGGCGCTCATCAAGTCGCCTA 228	35 CCACTCCCTCGGCCGCGGAGGCTGGCCGGCTGGCGGAAGGGCTGATCAAGTCGCCCA 94 229 AACCTCTGATGAAGAAGCAGGGGGGTGAAAGCACCATCACAAACACAACCTGCGGCACC 288	289 GCTACGAGTTCCTGGAGACGCTGGGCACCTACGGGAAGGTGAAGAAGGCACGAG 348 	349 AGAGCTCGGGGCGTCTGGTGGCCATCAGGAAAGACAAAATCAAAGATGAGC 408 	409 AGGATCTGCACATACGGAGGGAGATTGACATCTTCACTCAACCACCCCCACA 468	469 TCATTGCCATCCATGAAGTGTTTGAGAATAGCAGGATTGTGATTGTCATGGAGTATG 528 	529 CCAGCCGAGGCGATCTGTATCATTACATCAGTGAGCCGCCCGGCTGAGTGAG	
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Fod, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                1826 ACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGTCTGCTCAAAGCTCACCCT
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This sequence was made by sequencing genomic exons and order them based on alignment.

Location/Qualifiers
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                       BI653092 746 bp mRNA linear EST 12-SEP-2001
603300616F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5341299 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 746)
11 (hases 1 to 746)
12 (hac.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapba-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.I.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1866 row: p column: 04
High quality sequence stop: 746.
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/mol_type="markNa"
/strain="129, C57BL/6J, FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5341299"
/tissue_type="tumor, gross tissue"
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Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (Bases 1 to 795)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-rémail.nih.gov

Tissue Procurement: Dr. Jim Lin, Gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/Lin. at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                   Seq primer: pYX-5
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organism="Mus musculus"

/mol_type="mRNA" /strain="C57BL/6"

Location/Qualifiers

/db_xref="taxon:10090" /clone="IMAGE:6816569"

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/tissue type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab.host="whole Tri phage resistant"
/lab.host="DH10B (Tri phage resistant")"
/clone lib="WINH BMAP_FWO"
/clone lib="A library was constructed according Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarcas gel: First strand CDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand CDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pXX-Aso vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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CA319312
UI-M-FW0-cbz-i-16-0-UI.rl NIH BMAP_FW0 Mus musculus cDNA clone

CA319312 CA319312.1 GI:24537436

DEFINITION ACCESSION VERSION

RESULT 8 CA319312

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UI-M-HD0-clc-b-24-0-UI.rl NIH BMAP_HD0 Mus musculus cDNA clone MAGE:30615119 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nin.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                      CACGAGAGAGACTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAG 360
                                                                                                ATGAGCAGGATCTGCTGCACATACGGAGGAGGATTGAGATCATGTCTTCACTCAACCACC 420
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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CACGAGAGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAAGACAAAATCAAAG
                                                                                                                                                                                      CCCACATCATIGCCATCCATGAAGTGGGCAGATCACGCTTAGTGACTGTGTTTGAGAATA
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                                                                          ATGAGCAGGATCTGCTGCACATACGGAGGAGATTGAGATCATCTTCACTCAACCACC
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30615119"
/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
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AUTHORS
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KEYWORDS
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CF729223
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2487

629

PEATURES

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/lab host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HD0"
/clone_lib="NIH_BMAP_HD0"
Site_2: Not I; The library was constructed according
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarces
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I addaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATYGAAGT. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.6%; Score 714; DB 7; Length 727; llarity 99.6%; Pred. No. 3.4e-157; Conservative 0; Mismatches 2; Indels
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Mus musculus (house mouse)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 705)

RS MiH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                       2349
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UI-M-GZ0-cjp-h-08-0-UI.rl NIH BMAP GZ0 Mus musculus cDNA clone IMAGE:30606415 5', mRNA sequence.
                                                                                                           431
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                                                                                                                                           TGTGTAGTGACTGCCATTATTAGAGAAAACAGCCTCTGGTTTCCATCTGCTGCTG
                                                                                                                                                                                                                TGCATCTCAAAGACCTGGGAAGACTCGGACCGCTGTTTGACTTCATCTCAAGGGGACCAG
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                                                                                                                                                                                                                                                                                                                            ATGCCCCTGGA-CCCATCTTAGATCTCAGAGACTTGAACCTTGAAGCTGTTCCTAGTACC
                                                                                                                                                                                                                                                                                                                                                            2530 CAGATGTGGA-TGGATGCTCTGTTTCTCAGGCCAACGGGACCTAGAATGTGCTGACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2647 ITITIAAGTGAATTITGCT-GCTTTCAATAATGTGAATGCTGTGTTCTGGGGAACTCCAC
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CF726196.1 GI:37600364
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CF726196
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992 bp mRNA linear EST 05-JUN-2001
6021523111 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4937647 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 992)
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                                                                                                                                                                                                                                              1 (bases 1 to 992)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTAGGAATCTGCTCAAAGCTCAGCTCAGGAAGGAGAGATGGTGCCCTAGTATGGGGTAGG
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                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM10871 row: m column: 08
High quality sequence stop: 695.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.1%; Score 700.2; DB 4; Length 992; larity 92.2%; Pred. No. 6.6e-154; Conservative 0; Mismatches 60; Indels 12
                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
                                                                                                                                     BG915967.1 GI:14296443
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                                                                                                   mRNA sequence.
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Matches 857; Conserv
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                                                                               DEFINITION
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TITLE
JOURNAL
COMMENT
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BG915967
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KEYWORDS
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/db_xref="taxon:10090"
/clone="IMAGE:5718428"
/clone="IMAGE:5718428"
/clone="IMAGE:5718428"
/dab_host="whole brain"
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/note="Organ: brain; Vector: pXX-A8c; Site 1: EccR I;
Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-fT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator:"
                                                                                                                                                                                                                                                                                                         CB248251
UI-M-FD0-byi-a-21-0-UI.rl NIH_BMAP_FD0 Mus musculus cDNA clone
IMAGE:5718428 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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                                                                           613 GCCACCAGAACGGGATCGTTCACCGAGATCTCANGCTGGAANACATCCTTCTAGATGCCA 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus Sukaryota, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutheria, Musinae, Musinae, Musinae, Musinae, Lo. 726)
1 (bases 1 to 726)
11 (bases 1 to 726)
12 (bases 1 to 726)
13 (bases 1 to 726)
14 (bases 1 to 726)
15 (bases 1 to 726)
16 (bases 1 to 726)
17 (bases 1 to 726)
18 (bases 1 to 726)
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Best Local Similarity 98.8%; Pred. No. 5.1e-150;
Matcheg .720; Conservative 0; Mismatcheg 5;
                                                                                                                                                                                       705
                                                                                                                                691 ATGGAAACATCAAGATTGCTGACTTTGGCCTCT
                                                                                                                                                                673 NIGGAAACAICANGAITGCIGACIITGGNCICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
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AUTHORS
TITLE
JOURNAL
COMMENT
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CB248251
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                                                                                                                                                                                                                                /tissue type="whole eye"
/dev stage="embryo 12.5,13.5,14.5 dpc"
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/dore lib="MINH BMAP GZO"
/clone lib="MINH BMAP GZO"
/note="Organ: Eye; Vector: pXX- Asc; Site l: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcse
gel.First strand CDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand CDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
lowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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                                                                                                   'organism="Mus musculus"
                                                                                                                                                                                 db_xref="taxon:10090"
/clone="IMAGE:30606415"
                                                                                                                                'mol_type="mRNA"
'strain="C57BL/6"
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                                                                                              organism="Mus musculus"
                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
                                    Location/Qualifiers
            Seg primer: pYX-5
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UI-M-HUO-cqx-a-14-0-UI.x1 NIH BMAP_HUO Mus musculus cDNA clone
CQ424322
                                                         GTCAACTGGGGTTACACCACCGGAGTCGGGGAACAGGAAGCCCTGCGTGAGGGTGGGCAC 1100
                                                                                                                                                                             CCTAGTGGTGACTTTGGCCGGGCCTCCATGGCGGACTGGTTACGTCGCTCCTCGCGCCCC 1160
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Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
Http://genome.ulowa.edu/distribution/mousefi.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                           CCTAGTGGTGACTTTGGCCGGGCCTCCATGGCGGACTGGTTACGTCGCTCCTCGCGCCCC 240
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 672)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Itsue Procurement: Dr. James Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.ulowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The following repetitive elements were found in this cDNA sequence: 1-75, >POLY A#Simple_repeat (matched compliment) 297-361, c CAAA) n#Simple_repeat
Seq primer: pXX-3
POLYAAYes.
CTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGACGCCAGTGATG 660
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 716)
11 HMG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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TAG_SEQ=None found"
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/strain="C57BL/6"
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C0041415.1 GI:48581955
                                                    TGTTTGTGAGTG
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 986)

S NIH-MGC http://mgc.nci.nih.gov/.

I (bases 1 to 986)

National Institutes of Health, Mammalian Gene Collection (MGC)

LOnpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

Coffice of Cancer Genomics

National Cancer Institute / NIH

Bldg: 31 RalloA07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Geradwohl (PNAS 97 P1607-1611, 2000) CF584809

AGENCOURT 8798011_updated NIH_MGC_137 Mus musculus cDNA clone IMAGE:6431112 3', mRNA sequence. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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/folone lib= NIH MGC 137"

/note= "Organ: pancreas; Vector: pSPORT1; Site 1: Sall;

Site 2: Not1; Library consists of a pool of clones
rearrayed from the following libraries: Melton normalized
mixed mouse pancreas 1 N1-MMS1, Amplified Melton mouse
tislets 1 MIS1-A, and Kaestner ngal Wt. Clones rearrayed in
the laboratory of K. Kaestner (University of
Pennsylvania). Note: this is a NIH_MGC Library."
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DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRBD13 row: a column: 01
High quality sequence start: 95
High quality sequence stop: 347.
Location/Qualifiers
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Pred. No. 3.9e-145;
0; Mismatches 24;
                                                                                                                                                                                                                        organism="Mus musculus"
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/db_xref="taxon:10090"
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The present sequence is Murine Lymph node Stromal cell kinase I (MLSK-1). This protein is useful for treating a variety of disorders listed in the disclosure of the specification, including autoimmune disorders, allergic reactions, myeloid or lymphoid cell deficiencies, wound healing and tissue repair and replacement, burns, incisions and ulcers, periodontal disease, inflammatory diseases, tumours and bacterial, viral or fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses.
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                   GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
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Post-processing:

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                                                                                                                                  ETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIH 120
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                                                                        1 MESVALLQRPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL
                                                                                                                                                                EVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDL
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                                            MESVALLORPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL
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/note= "Protein kinase ATP-binding region signature"
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700ce "Serine/threonine protein kinase active-site"
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70ote= "Serine/threonine kinase catalytic domain"
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100.0%; Pred. No. 9.5 ive 0; Mismatches
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              631; Conservative
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The invention relates to an AMPK (AMP-activated protein kinase)-related
kinase designated SNARK polypeptides and polynucleotides. SNARK
(SNIF/AMP-activated protein kinase) is involved in stress response to
glucose deprivation. The polynucleotides are useful for expressing SNARK
protein in isolated form or as a protein conjugate. Activation of SNARK
confinitates liver CPT-1 thus enhances lipid metabolism in liver cells and
in other cell types such as heart and sheletal muscles, as well as
in other cell types such as heart and sheletal muscles, as well as
increases GLUT-4 and glycogen in muscle. Activation of SNARK is predicted
in other cell types such as leart and sheletal muscles, as well as
increases GLUT-4 and glycogen in muscle. Activation of SNARK is predicted
to have insulin-like effects that would enhance the disposal of glucose
to have insulin-like effects that would enhance the disposal of glucose
conne type of disorders of lipoprotein production leading to increased
some type of disorders of lipoprotein production leading to increased
levels of cholesterol or triglycerides. SNARK or its variants may be
administered to a subject to treat or prevent a disease associated with
decreased expression of SNARK, such as diabetes. SNARK antibodies are
used to modulate SNARK activity either in vivo for therapeutic purposes.
SNARK antagonists may be administered to increase fuel production,
decrease glucose uptake and increase levels of blood glucose in a patient
suffering from hypoglycaemia. The present sequence is rat SNARK protein
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             /note= "Serine/threonine kinase catalytic domain"
381. .384
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                                                                                                                                             517. .520
/note= "Serine/threonine kinase catalytic
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                                                    /note= "Serine/threonine kinase catalytic
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/note= "Serine/threonine
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12-MAR-2001; 2001US-0274613P.
28-MAR-2001; 2001CA-02340783.
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Matches 593; Conservative
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        The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length cDness were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did format directly from EPO
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Best Local Similarity 85.7%; Pred. No. 1.9e-239;
Matches 544; Conservative 26; Mismatches 54;
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ABU53319
ID ABU5:
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T, Koga
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S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA; cDNA synthesis; oligo-capping
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K, Kojima (
                                                                                                                                                                                                                                                                                                                                       ESLGDSCFSLTDCQEVTAAYRQALGICSKLS
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Wakamatsu A, Sugiyama T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide, SEQ ID NO:
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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N-PSDB; AAK94280.
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  |: ||||| || ||: ||| || || || || || ||| ||| ||| ||| ||| ||| ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || 
                                                                                                       AGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRPL 533
                                                                                                                                                                                                    ARASRPSGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEEPPSEGPGSCLR 593
                                                                                                                                                                         ARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSVDNLRGLEQPPSEG----LK 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; multiple sclerosis; dimunomodulator; nootropic; neuroprofective; arthritis; cytostatic; immunomodulator; nootropic; neuroprofective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polynucleotide (1) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ren
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Ghosh 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a polypeptide described in the disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies.
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                                              Human; gene therapy; vaccine; disease treatment; detection
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cell cycle-associated protein from DKFZphtes3_7j3
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85.7%; Pred. No. 1.9e-239;
ive 26; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                     (GEHU-) GERMAN HUMAN GENOME PROJECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 21; Page 943; 1095pp; English.
                                                                                                                                                                                                                                      2000WO-IB001496.
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Best Local Similarity 85.7
Matches 544; Conservative
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28-SEP-1999;
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25-SEP-2000; 2000US-0234922P 25-SEP-2001; 2001WO-US030115

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Homo sapiens.

(MILL-) MILLENNIUM

Galvin KM;

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or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                   Gaps
                                                                                                                                   11;
                                                                                                    85.8%; Score 2824.5; DB 5; Length 628;
85.7%; Pred. No. 1.9e-239;
ive 26; Mismatches 54; Indels 11;
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                                                                                                                                Conservative
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                                                                        Sequence 628 AA;
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Best Local Simil
Matches 544; C
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The present invention relates to the isolation of a novel human protein
kinase designated 3700, and the polynucleotide sequence encoding it. The
invention also describes the use of a modulator of the activity of
protein kinase (PK) 3700 for making a medicament or pharmaceutical
composition for modulating the ability of a cell to phosphorylate an
enino acid residue of a substrate protein. Modulators of protein kinase
composition for modulating the modulating protein phosphorylation, cell
signalling, tumourigenesis, mitogenesis, transcription of a gene,
angiogenesis, tissue repair, tissue regeneration, establishment or
composition of atherosele. mitogenesis, transcription of a gene,
angiogenesis, tissue repair, tissue regeneration, establishment or
composition of atherosele. and polypeptide molecules for protein kinase
compositioning, diagnosing, preventing, inhibiting, alleviating, or
curing Pk-related disorders and cellular proliferative and/or
curing Pk-related disorders and cellular proliferative and/or
curing excoma, metastatic disorders or leukaemia). The 3700
curing carcinoma, sarcoma, metastatic disorders or leukaemia). The 3700
carcinoma, sarcoma, metastatic disorders or leukaemia). The 3700
cetect a genetic alteration in a 3700 gene, in chromosome mapping, for
tissue typing, in forensic biology, and as surrogate markers. The present
sequence represents human protein kinase 3700
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                                                                                                                                                                                                                                                                                                                                                          Use of modulators of activity of 3700 protein for making medicament f
e.g., modulating protein phosphorylation or cell signaling, or for
treating or preventing cellular proliferative and/or differentiative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 19; Fig 1; 115pp; English.
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Les 544; Conservative
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N-PSDB; ABK14000.
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Human, protein kinase 3700; PK, protein phosphorylation; tumourigenesis; cell signalling, mitogenesis; gene transcription, angiogenesis; sarcoma; tissue repair; tissue regeneration; atherosclerosis; blood-brain barrier; cell proliferation disorder; cell differentiation disorder; carcinoma; haematopoietic neoplastic disorder; metastatic disorder; leukaemia; cytostatic; antiatherosclerotic; enzyme.

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                                                                                                                                                          297 VASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLLENGAKVCSFFKQ 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel nucleic acids encoding human PRO secreted
                                                                     ASDVFVSGDPVEQKSPQASGLLLHRKGILKLNGKFSRTALEGTTPSTFGSLDQLASSHPA
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                                                                                                                                 TSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPSESGELLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New PRO polypeptides, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; oytotoxac factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane bound protein; membrane bound receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human secreted and transmembrane protein SeqID 640.
                                                                                                                                                                                                                                                                                                                                                                                                      631
                                                                                                                                                                                                                                                                                                                                                                                                                           RWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS
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N-PSDB; ADF76964.
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Williams PM,
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cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the CDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present
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                                                                                                                                                                                                                                                                                                                                Query Match
85.8%; Score 2824.5; DB 7
Best Local Similarity 85.7%; Pred. No. 1.9e-239;
Matches 544; Conservative 26; Mismatches 54;
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                                                                                                                                                                                                                                                   invention.
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ADL30886
ID ADL3
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AC ADL3
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DT 20-M
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Human protein encoded by a full length cDNA clone SeqID 2919.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agent for imparting stress resistance to cells, comprises DNA encoding for adenosine monophosphate activated protein kinase-related kinase 5 ftreatment of tumors, muscle and nervous disorders, and ataxia
                                                                                           AGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRPL
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                      ASAEGVQEDPPELSPIPASPGQAAP---LLPKKGILKKPRQRESGYYSSPEPSESGELLD
                                                                      ASDVFVSGDPVEQKSPQASGLLLHRKG1LKLNGKFSRTALEGTTPSTFGSLDQLASSHPA
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                                                                                                                                                        TSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPSESGELLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; Neuroprotective; Nootropic; Muscular; Gene therapy; defensalme Monophosphate activated Protein Kinase-related kinase 5; AMK5; AIRAO 537; stress resistance; tumour; nervous disorder; muscie disorder; ataxia teleangiectasia; SNARK.
                                                                                                                                       ARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSVDNLRGLEQPPSEG
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85.7%; Pred. No. 1.9e-239;
ive 26; Mismatches 54;
                                                                                                                                                                                                         631
                                                                                                                                                                                                                       RWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS
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(PHAR-) ORG PHARM SAFETY & RES.
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                                                                                                                                                                                                                                                                                                                          standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Human SNARK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Best Local Simil
Matches 544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polypeptide sequence is a full length human protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VASHWWYNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLLENGAKVCSFFKQ 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAPGGGSTTPGLERQHSLKKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPKGILKKKVS 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MESVALLORPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL 60
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human, medicine; signal transduction; glycoprotein; transcription;
oligo-capping method.
                                                                                                                                                                                                                                                                                                        Kawai Y;
T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                          oligonucleotide primers (830 cDNAs) useful for synthesizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Indels
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S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.8%; Score 2824.5; DB 885.7%; Pred. No. 1.9e-239; ive 26; Mismatches 54;
                                                                                                                                                                                                                                                                                                      Hayashi K,
K, Kojima (
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 2919; 1340pp; English
                                                                                                                                                                                                                                                                                                   Ota T, Nishikawa T, Isogai T,
Wakamatsu A, Sugiyama T, Nagai
                                                                                                                                                                                                                                                                     (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                  11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
                                                                                                                                                   07-JUL-2000; 2003EP-00025638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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N-PSDB; ADL30885.
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US2004058355-A1 Homo sapiens

25-MAR-2004

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KLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVDSWSL 236
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ETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory disorder; cardiovascular disorder; disease; pain disorder; metabolic disorder; liver disorder; viral disease; pain disorder; metabolic disorder; neurological disorder; sorder; central nervous system disorder; erythroid disorder; blood vesel disorder; angiogenic disorder; cancer; heart failure; hypertension; angina; osteoarthritis; rheumatoid arthritis; multiple solerosis; Crohn's disease; psoriasis; aschma; cell proliferation; cell differentiation; cell growth; cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; cardiant; hypotensive; antianginal; osteopathic; antiarcheumatic; neuroprotective; antiaflammatory; antiarchmatic; antiarchmatic; cardiovascular; virucide; analgesic; antiarchmatic; cardiovascular; virucide; analgesic; cospenseis inhibitor; angiogenesis stimulator; cerebroprotective; nephrotropic; antithyroid; dermatological; immunomodulator; cell proliferation disorder; cell differentiation disorder; brain disorder; brain disorder; breast disorder; colon disorder; kidney disorder; renal disorder; breast disorder; cervical disorder; spleen disorder; thymus disorder; thyroid disorder; eervical disorder; spleen disorder; thymus disorder; pancreatic disorder; skeletel muscle disorder; skin disorder; dermal disorder; immune disorder;
                                                                       EVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDL
                                                                                                                                              KLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL
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Meyers RE, Rudolph-Owen LA;
Galvin KM, Chun M, Williamson MJ;
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Curtis RAJ, Olandt PJ, Tsai F,
Silos-Santiago I, Bandaru R;
                                                                                9905-00365162
9905-00392189.
9905-00448076.
200005-0186061P.
200005-0200688P.
200005-0200688P.
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2000US-00711216.
2000US-0248325P.
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2001US-00909743
2001US-00920346
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2001US-00929218
2001US-0312539P
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2000US-0235035P
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2002US-00121911
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                                                25-APR-2003; 2003US-00423543
                                                                                                                                  2000US-00608921
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                                                                                         09-SEP-1999
                                                                                                                                                                                                                                                                             5-NOV-2001
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The invention describes an isolated 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 2644, 56638, 18610, 33217, 1967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising any one of 40 nucleotide sequences (I). The nucleic acid molecules and polypeptides are useful for diagnosing and treating a subject having a disorder, or a subject at risk of developing a disorder, which is associated with aberrant 21910, 56634, 55053, 2564, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 activity, such as cellular proliferative and/or

New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecules and proteins, useful for treating, e.g. cancer, heart failure and angina.

WPI; 2004-268788/25. N-PSDB; ADL14160, ADL14162.

Claim 4; SEQ ID NO 44; 139pp; English.

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disorders, colon disorders, kidney (renal) disorders, lung disorders, ovarian disorders, prostate disorders, cervical disorders, lung disorders, ovarian disorders, prostate disorders, cervical disorders spleen disorders, thywing disorders, testes disorders, chamatopoietic disorders, thywing disorders, skeletal muscle disorders, skin (dermal) disorders, disorders associated with bone metabolism, immune, e.g. inflammatory disorders, cardiovascular disorders, candorhelial cell disorders, liver disorders, viral diseases, pain disorders, endothelial cell disorders, liver disorders, viral diseases, pain disorders, endothers, erythroid disorders, blood vessel disorders or angiogenic disorders (all claimed), e.g. cancer, heart failure, hypertension, cangina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease, psoriasis, or asthma. The nucleic acid molecules and collises are also useful as modulating agents in regulating a variety of cellular process, e.g. cell proliferation, differentiation, growth and division. This is the amino acid sequence of a novel human protein of the invention. Note: The sequences given in the specification are also
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differentiative disorders, brain disorders, platelet disorders, breast
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ilarity 85.7%; Pred. No. 1.9e-239;
Conservative 26; Mismatches 54;
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Best Local Similarity
Matches 544; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for ing an immune related disorder such as systemic lupus erythematosus, atoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                            rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogram's syndrome, vasculitis, sarchifis, systemic haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central tor peripheral mervous system, demyelinating diseases of the Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy, polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MESVALLQRPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL
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                                                                                                                                  disorder; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams PM;
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ADO20172 standard; protein;
                                                                                                                                related
                                                                                              Human PRO polypeptide #540
                                                               (first entry)
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                                                                                                                                                                                                                                                                                 Homo sapiens
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Best Local Simi:
Matches 544;
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                                                                         VASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFKQ 360
                                                                                                                                                                                                           AGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRPL 533
                                                                                                                                                                                                                                 ARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSVDNLRGLEQPPSEG----LK 596
                                                                                                                                                                                                                                               ARASRPSGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEEPPSEGPGSCLR 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule encoding a kinase polypeptide, useful for preparing a composition for treating diseases or disorders, e.g., cancer, or neurological, immunological or inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                 Human calcium/calmodulin-dependent protein kinase NuaK2 protein SeqID 77
                                                                                                                                                                                                                                                                                                                                                                                                                 kinase; human; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease; cardiovascular disease; brain; neuronal associated disease; metabolic; inflammatory disorder; cytostatic; neuroprotective; immunomodulator; antiinflammatory; enzyme; calcium/calmodulin-dependent protein kinase;
         KLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVDSWSL
                                              GVLLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED
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                                                                                                               HVPGGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKSS
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N-PSDB; ADJ96554.
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This invention relates to a novel isolated, enriched or purimical acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinase [PTK's and STK's], as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, and targonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cycostatic, neuroprotective, immunomodulator and antinflammatory according a human kinase protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                        DVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFK
                                                                                                         DVASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLLENGAKVCSFFK
                                                                                                                                                           QHVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKS
GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; antisense gene therapy; MARK3;
MAP/microtubule affinity-regulating kinase 3; ca
Alzheimer's disease; neurodegenerative disorde;
hyperproliferative disorder; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-052188/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigans in the production of antibodies of kinase expression and activity. Anti-kinase antibodies of and kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplanteation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
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                                                   Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers.
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                  SEQ ID NO:
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                protein kinase,
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                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFK 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLLENGAKVCSFFK 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the expression of MARK3 in cells or tissues, treating an animal having can suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonuclectide is useful for preparing a composition for treating hyperproliferative discorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated protein included in the figures but not mentioned anywhere else in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPSESGELL
                                                                                                                                                                                                                                   MESVALLQRPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL
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                                                                                                                                                                         Length 629;
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Pred. No. 2.8e-237;
6; Mismatches 56;
                                                                                                                                                               85.2%; Scor
85.2%; Pred
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                                                                                                                                         Sequence 629 AA;
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                                                                                                                                                                  Query Match
Best Local Simi
Matches 542;
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The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition containing PKIN agonist is useful for treating a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disorders include cancer (leuksemia, adenocarcinoma, lymphoma, melanoma, allergies, adult respiratory distress syndrome, autocimmune thyroiditis, gout, bronchitis, crohn's disease, diabetes autoimmune thyroiditis, osteoparosis, Good pasture's syndrome, Graves' disease, costeoarthritis, osteoparosis, pancreatitis, pancriatis, pacciasis, cirrhosis, crhoumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis, bacterial, parasitic, fungal, viral, protezcal and helminthic infections) crowling's syndrome, hypothyroidism, cerebral palsy, cataracts), cardio vascular disease (arteriovenous fishula, hypertension, vasculitis, circhaemic heart failure, angina pectoris, myccarditis, is caneurysms, congestive heart failure, angina pectoris, myccarditis, is chancemic heart disease, chronic bronchitis, lung tumoure); lipid disorder (fatty liver, Palvy's disease, Niemann-Pick's disease, hypochity, hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity Human, kinase, PKIN-12; cancer, leukaemia, adenocarcinoma, osteoporosis, immune disorder, atherosclerosis, Crohn's disease, Hodgkin's disease, Acquired Immune Deficiency Syndrome, AIDS; Addison's disease, anaemia, 594 Human kinase PKIN-12 protein. AAE16266 standard; protein; (first entry)

26-MAR-2002

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AAE16266;

AAE16266

New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.

WPI; 2002-090207/12. N-PSDB; AAD26459.

Claim 1; Page 152-153; 197pp; English

Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y; Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR; Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT; Bughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R; Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L; Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;

(INCY-) INCYTE GENOMICS INC.

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allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis; Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris; cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; congestive heart failure; ischaemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy.
                                                                                                                                                                                                                                                                                                                                                /note= "Eukaryotic protein kinase domain"
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2000US-0213467P.
2000US-0215651P.
2000US-0216605P.
2000US-0218372P.
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23-JUN-2000;
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                                                                                                                                                                              DACGLIRWILMVNPTRRATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMAD 338
                                                                                                                                                                                                               TSSRPGKSSLKLPKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKK 458
                                                                      VSVDNLRGLEQPPSEG----LKRWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
of a test compound and in gene therapy. The present sequence is human {\tt PKIN-12} protein
                                       Query Match 82.6%; Score 2720.5; DB 5; Length 594;
Best Local Similarity 87.3%; Pred. No. 2.6e-230;
Matches 521; Conservative 22; Mismatches 47; Indels 7; Gaps
                         Sequence 594 AA;
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Sequence 11, Appl
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Sequence 38, Appl
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RESULT 1 US-09-579-664B-11 Sequence 11, Application US/09579664B Patent No. 6514719 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Immunex Corporation APPLICANT: Bird, Timothy A. APPLICANT: Wire, G. Duke APPLICANT: Martin, Unja APPLICANT: Anderson, Dirk M. TITLE OF INVENTION: NOVEL MURINE AND HUMAN FILE REFERENCE: 2923-4 CURRENT APPLICATION NUMBER: US/09/579,664B CURRENT FILING DATE: 2000-05-26 SOFTWARE: PATENTING DATE: 2000-05-26 SOFTWARE:	Query Match Best Local Similarity Matches 631; Conser						
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  361 HVPGGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKSS 420
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Sequence 38, Application US/10355975A

Patent No. 675923

GENERAL NO. 675923

GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Bird, Timothy A.
APPLICANT: Mirca, G. Duke
APPLICANT: Arctin, Unja

APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
FILE REFERENCE: 2923-B

CURRENT APPLICATION NUMBER: US/10/355,975A

CURRENT FILING DATE: 2003-01-30

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin Version 3.1

SEQ ID NO 38
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HVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKSS 420
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                                TSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPSESGELLD
                                                                                                                                  TSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPSESGELLD
                                                                                                                                                                                                                                                                                                                                               ASDVFVSGDPVEQKSPQASGLLLHRKGILKLNGKFSRTALEGTTPSTFGSLDQLASSHPA
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| Patent No. 675923
| GENERAL INFORMATION:
| APPLICANT: Immunex Corporation
| APPLICANT: Immunex Corporation
| APPLICANT: Immunex Corporation
| APPLICANT: Wired, G. Duke
| APPLICANT: Marchin, Unja
| APPLICANT: Maderson, Dirk M. |
| TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
| FILE REPERENCE: 2923-B
| CURRENT APPLICATION NUMBER: US/10/355,975A
| CURRENT APPLICATION NUMBER: US/10/355,975A
| NUMBER OF SEQ ID NOS: 38
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO ID NO ID NOS: 38
| SOFTWARE: PatentIn version 3.1
| TEMPTHY OF TABLET |
| TEMPT
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100.0%; Pred. No. 2.2e-277;
ive 0; Mismatches 0;
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ORGANISM: Mus musculus
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US-10-355-975A-11
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OY 421 TSSGEVOEDPOELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPGESGELLD 480		<i>ك</i> 8	236 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYBEPPKPSDAC-GLIRWLLMVNPTR 294	
QY 481 ASDVFVSGDPVEQKSPQASGLLLHRKGILKLNGKFSRTALEGTTPSTFGSLDQLASSHPA 540		\$ a	295 RATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGPFGRASMADWLRRSSRPLLENGAKV 354	
QY 541 ARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSVDNLRGLEQPPSEGLKRWWQ 600		& 8	355 CSFFKQHVPGGGSTVPGLERQHSLKKSRKENDMQNLQGDPAEDTSSRPGKSSLKLP 411	•
QY 601 ESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631		දු පු	412 KGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGIL 456 (1873年) 1	指指
RESULT 4 US-08-677-298-2 ; Sequence 2, Application US/08677298 ; Patent No. 5863729		ò a ò	457 KKSRQRESGYYSSPEPSESGELLDASDVFVSGDPVEQKSPQ 497 :	
; GENERAL INFORMATION: ; APPLICANT: Piwnica-Worms, Helen ; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAK-1 ; TITLE OF INVENTION: KINASE		· 셤 상	:	
; NOMBER OF SECTION 1 / CORRESPONDENCES: 1 / CORRESPONDENCES: 1 / ADDRESSEE: Greenlee, Winner and Sullivan, P.C. : STREET: 5370 Manhattan Circle. Suite 201		qq	549 TPDRIRFPRGTASRST 564	
Y: Boulder IE: CO NTRY: USA		RESULT 5 US-09-523-849-33 ; Sequence 33, A	SULT 5 -09-523-849-33 Sequence 33, Application US/09523849	
; ZIP: 80303 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk		; Patent No. ; GENERAL INI ; APPLICANT	Patent No. 6458561 GENERAL INFORMATION: APPLICANT: Bandman, Olga	
; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA:		APPLIC APPLIC APPLIC APPLIC APPLIC	APPLICANT: Molteni, Angela APPLICANT: Magnaghi, Paola APPLICANT: Bosotti, Roberta APPLICANT: Scacheri. Emanuela	
APPLICATION NUMBER: US/08/677,298; FILING DATE: 09-JUL-1996; CLASSIFICATION: 536		APPLIC APPLIC TITLE	ANT: Isacchi, Antonella ANT: Hodgson, Dave OF INVENTION: HUMAN NIM1 KINASE	
; ATTORNEY/AGENT INFORMATION: ; NAME: Caruthers, Jennie M: ; REGISTRATION NUMBER: 34,464 ; REFERENCE/DOCKET NUMBER: 9-96		; FILE R; CURREN; CURREN; NUMBER	FILE REFERENCE: PC-0009 US CURRENT APPLICATION NUMBER: US/09/523,849 CURRENT FILING DATE: 2000-03-13 NUMBER OF SEQ ID NOS: 39	
TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 499-8080 TELEFAX: (303) 499-8089		SOFTWARE SEQ ID NO LENGTH:	FTWARE: PERL Program ID NO 33 ENGTH: 729	Pro-
; INFORMATION FOR SEQ ID NO: 2: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 729 amino acids . TYPE: amino acids		; TYPE: PR ; ORGANISM ; FEATURE: ; NAME/KEY		: 3.
; TOPOLOGY: Inear; ; MOLECULE TYPE: protein US-08-677-298-2		OTHER US-09-523	OTHER INFORMATION: GenBank Accession No. 6458561 g3089349	
Query Match 21.4%; Score 703.5; DB 2; Length 729; Best Local Similarity 35.1%; Pred. No. 3.4e-52. Matches 106. Concernative 76. Mismatches 100. Indels 106. Cans 18.		Query Match Best Local 8 Matches 199	atch 21.4%; Score 703.5; DB 4; Length 729; cal Similarity 35.1%; Pred. No. 3.4e-52; 195; Conservative 76; Mismatches 180; Indels 105; Gaps 18;	
57 YEPLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLHIRREIEIMSSLNHPH 1		ò a	57 YEPLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH 115 : : :	
SO YKLLKTIGKGNFAKVKLAKHILIGKEVAIKIIDKIQL-NPISLQKLFKEVKIMKLLNHFN 116 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI : :	· f	à a	116 IIAIHEVPENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFRQIVSALHYCHQNGI 175 	
115 IVKLFEVIEIEKILYLIMEYASGGEVFDYLVANGKRKEKEAKSKFKQIVSAVQYCHUKKI 176 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV		<u>ک</u> ۾	176 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 235	
Db 175 VHRDLKAENLLLDADMNIKIADFGFSNEFTVGGKLDTFCGSPPYAAPELFQGKKYDGPEV 234		ò	236 DSWSLGVLLYILVHGTMPPDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTR 294	

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57 YEFLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH 115
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                                                                                                                             : | : | : | : | : | : | 337 GMGYSQB------EIQESLSKOMKYDEITATYLLLGRKSSEVRPSSDLNNSTGQS- 384
                                                                                                                                                                                                                                                                            434 ISSRKSTGSAVGCKGIAPASPM--LGNASNPNKADIPERKKSSTV-----PSSNTAS 483
                                                                                                                                                                                                                                                                                                                                               GGMTRRNTYVCSERTTDDRHSVIQ-NGKENSTIPDQRTP-----VASTHSISSAATP 534
                                                                                                        ---- QGDPAEDISSRPGKSS 407
                                                                                                                                                                                                                ---PHHKVQRSVSSS------QKQRRYSDHAGPGIPSVVAYPKRSQTSTADSDLKEDG 433
                                                                                                                                                                                                                                                   -----KGILKKSRQRESGYYSSPEPSESGELLDASDVFVSGDPVEQKSPQAS 499
                                                                                                                                                                                                                                                                                                                        -----GILKLNGKFSRTALEGTTPSTFGSLDQLASSH---PAARP 543
 DVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFLVLNPIK 294
                                   RATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKV 354
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NAME/KEY: misc_feature
OTHER INFORMATION: GenBank Accession No. 6458561 g2052189
                                                                     RGTLEQIMKDRWINAGH-----BEDELKPFVEPELDISDQKRIDIM-
                                                                                                                                                                              408 LKLPKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPR
                                                                                                       355 CSFFKQHVPGGGSTVPGLERQHSLKKSRKENDMAQNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.0%; Score 691.5; DB 4; 35.6%; Pred. No. 4.3e-51; tive 76; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bosotti, Roberta
APPLICANT: Scacheri, Roberta
APPLICANT: Scacheri, Emanuela
APPLICANT: Hadgschi, Antonella
APPLICANT: Hodgsch, Dave
TITLE REFERENCE: PC-0009 US
CURRENT APPLICATION NUMBER: US/09/523,849
CURRENT FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32, Application US/09523849 Patent No. 6458561
                                                                                                                                                                                                                                                                                                                                                                                                                                   548
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ORGANISM: Rattus norvegicus
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Best Local Similarity 35.6*
Matches 187; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VHRDLKAENILLIDADMNIKIADFGFSNEFTVGGKLDTFCGSPPYAAPELFOGKKYDGPEV 234
                                                                                                                                                     337 GMGYSQE------EIQESLSKMKYDEITATYLLLGRKSSELDASDSSSSNLSLA 385
                                                                                                                                                                                                 KGILKKKSSTSSGE----VQ---EDPQELRPVPDTPGQPVPAVSLLPRK-----GIL 456
                                                                                                                                                                                                                                                                      KK---SRQRES------GYYSSPEPSESGELLDASDVFVSGDPVEQKSPQ 497
                                                                                                                                                                                                                                                                                                                                                                               498 ASGGMTRRNTYVCSERTTADRHSVIQ-NGKENSTIPDQRTP-----VASTHSISSAA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTR 294
RATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKV 354
                                                                                                                           CSFFKQHVPGGGSTVPGLERQHSLKKSRKENDMAQNL---QGDPAEDTSSRPGKSSLKLP 411
                                                                                                                                                                                                                                                                                                                                             -----GILKLNGKFSRTALEGTTPSTFGSLDQLASSH---PAA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Giot. Loic
APPLICANT: Giot. Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15566-54
CURRENT APPLICATION NUMBER: U5/09/538,092
CURRENT PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR PLING DATE: 1999-04-01
PRIOR PLING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NOS: 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.1%; Score 694.5; DB 4; Length 713; 34.5%; Pred. No. 2e-51; ive 75; Mismatches 171; Indels 117;
                                                                            FEATURE:

NAME/KEY: misc feature

LOCATION: (0)...(0)

OTHER INFORMATION: Polypeptide Accession Number P27448
US-09-538-092-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5-09-538-092-1022
Sequence 1022, Application US/09538092
Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                                                                  542 RPSR---PSGAVSEDS 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                      549 TPDRIRFPRGTASRST 564
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191; Conservative
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Best Local S:
Matches 191
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CSFFKQHVPGGGSTVPGLERQHS	SULT 9 -09-984-890- Sequence 2, Patent No. 6 FREEL INC. APPLICANT: TITLE OF IN	Query Match Best Local Similarity 32.0%; Pred. No. Matches 201; Conservative 99; Mismatc Qy 6 LLQRPSQAPSASALASESARPLADGLIKS! Db 11 LNERDTEQPTLGHLDS	Qy 61 ETLGKGTYGKVKKARE-SSGRLVALKSIRI	Qy 120 HEVFENSKIVIVMEYASRGDLYDYISERI	OY 180 LKLENILLDANGNIKIADFGLSNLYHKGKE	Qy 240 LGVLLYILVHGTWPFDGQDHKTLVKQISNC		Oy 359 KQHVPGGGSTVPGLERQHSLKKSRKENDM2 :::
	A MO	; SEQ ID NO 36; ; LENGTH: 745; ; TYPE: PRT ; ORGANISM: Homo sapiens; ; FEATURE: ; NAME/KRY: misc feature ; OTHER INFORMATION: GenBank Accession No. 6458561 g1749794	Query Match 20.9%; Score 688; DB 4; Length 745; Best Local Similarity 32.9%; Pred. No. 7.8e-51; Matches 185; Conservative 89; Mismatches 192; Indels 96; Gaps 17;	QY 57 YEFLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH 115 	Qy 116 IIAIHEVPENSSKIVIVMEYASRGDLYDYISERPRLSERDAHFFRQIVSALHYCHQNGI 175 ::	OY 176 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLOTFCGSPLYASPEIVNGKPYVGPEV 235	236	QY 295 RATLEDVASHWWYNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKV 354

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1. 3.7e-50;
trches 195; Indels 134; Gaps 25;
                                                                      QAGPAIPTSNSYSKKTQSNNAENKRPEEDRES 409
                                                                                                         KSRQRESGYYSSPEPSESGELLDASDVFVSGD 489
                                                                                                                          TALEGITPSIFGSLDQLASSHPAARPSRPSGA 549
                                                                                                                                                                                   || ::||
TASASAAVSAARPRQHQKSMSASVHPNKASGL 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKDKIKDEQDLLHIRREIEIMSSLNHPHIIAI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :: : | : | | | | | | | | : : : DKTQL-NSSSLQKLFREVRIMKVLNHPNIVKL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFLQTFCGSPLYASPEIVNGKPYVGPEVDSWS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGAYREPPRESDAC-GLIRWLLMVNPTRRATL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSGDFGRASMADWLRRSSRPLLENGAKVCSFF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MA------QNLQGD------PAED-TSS 401
                 ------LKKKSSTSSGE---VQEDPQE 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KENDMA------DNLQGD-----PAED 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPKPLMKKOAVKRHHHKHNLRHR-----YEFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KPSSKSNMIRGRNSATSADEQPHIGNYRLL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                    90
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Qy	RESULT 11 US-09-984-890-4 i Sequence 4, Application US/09984890 i FILE PREMATION: i TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES i TITLE OF INVENTION: THERROF i TITLE OF INVENTION: THERROF i TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, i TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, i TITLE OF INVENTION: 1004/09/984,890 CURRENT FILING DATE: 2001-10-31 NUMBER OF SEQ ID NOS: 4 i SEQ ID NO 4 i LENGTH: 722 i TYPE: PRT CORGANISM: Rattus norvegicus US-09-984-890-4	; 5; Gaps	OY 6 LLORPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL 60 :		Qy 120 HEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFPRQIVSALHYCHQMGIVHRD 179	QY 180 LKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWS 239	OY 240 LGVLYTLVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATL 298	Qy 299 EDVASHWWVNMGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFF 358	Qy 359 KQHVPGGGSTVPGLERQHSLKKSRKENDWAQDLQGDPAEDTS 400	Qy 401 SRPGKSSLKLPKGILKKKSSTSSGEVQEDPQELRPVPDTPQQPVPAVSLLPRKGILKKSR 460	Qy 461 QRESGYYSSPEPSESGELLDASDVFVSGDP-VEQKSPQASGLLL 503 SinnaenkrPeeetgrkasstakVPasplPglDrkkttpptpstnsvlststnrsrnspll 486 427 QSNNAENKRPEEETGRKASSTAKVPASPLPGLDRKKTTPTPSTNSVLSTSTNRSRNSPLL 486
Qy 402 RPGKSSLKLPKGI		; LENGTH: 724 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-274-194-2	Query Match Best Local Similarity 32.0%; Pred. No. 3.7e-50; Matches 201; Conservative 99; Mismatches 195; Indels 134; Gaps 25;	QY 6 LLORPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYBFL 60 : :	QY 61 ETLGKGTYGKVKKARE-SSGRLVAIKSIRKOKIKDEQDLLHIRREIEIMSSLMPHIIAI 119 	Qy 120 HEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRD 179	Qy 180 LKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWS 239	Qy 240 LGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATL 298 [: : : Db 236 LGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKKFLILNPSKRGTL 295	QY 299 EDVASHWWVNGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFF 358	Qy 359 KQHVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAED-TSS 401 :::	402 RPGKSSLKLPKGILKKKSSTSSGEVQEDPQELRPV

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57 YEFLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSWSLGVLLY1LVHGTMPFDGQDHKTL-VKQISNGAYREPPKPSDAC-GLIRWLLMVNPT 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV
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                                                                                                                                                                                                                                                                                                  & Borun
                                                                                                                                                                                                         APPLICANT: MANDELKOW, Eckhard, et al.
TITLE OF INVENTION: No. 6579691el Protein Kinase
NUMBER OF SEQUENCES: 32
CORRESONDENCE ADDRESS:
ADDRESSEE: Maraball, O'Toole, Gerstein, Murray
STREET: 233 S. Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.5%; Score 675; DB 4; L 35.4%; Pred. No. 1.1e-49; tive 75; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/04258
FILING DATE: 30-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP 94 11 7122.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/817,832B
FILING DATE: 28-APR-1997
                                                                                                                                                Sequence 31, Application US/08817832B
Patent No. 6579691
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11
FILING DATE: 28-OCT-1994
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 779 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 35.4
Matches 186; Conservative
    559 --ESFDQLDLP 567
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                              : || :||
545 LRQVRDQQNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC of OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                    STREET: 233 S. We
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
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S ENCODING HUMAN KINASE PROTEINS, AND USES
                            487 DRASLGQASIQNGKDS-TAPQ-RVPVASPSAHNISSSSGAPDRINFPRGVSSRSTFHAGG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRESGYYSSPEPSESGELLDASDVFVSGDP-VEQK----SPQASGL------LL 503
504 HRKGILKL---NGKFSRTALEGTTPSTFGSLDQLASSHPAA-RPSRPSGAVSEDSILSS- 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFROIVSALHYCHONGIVHRD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KOHVPGGGSTVPGLEROHSLKKSRKENDMA-----ONLOGD-----PAED--TS 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRPGKSSLKLPKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSR 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSNNAENKRPEEETGRKASSTAKVPASPLPGLDRKKTTPTPSTNSVLSTSTNRSRNSPLL 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRKGILKL----NGKFSRTALEGTTPSTFGSLDQLASSHPAA-RPSRPSGAVSEDSILSS- 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLQRPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHR----YEFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.6%; Score 677.5; DB 4; Length 722; 32.9%; Pred. No. 6.1e-50; ive 92; Mismatches 203; Indels 115;
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PRO
TITLE OF INVENTION: ALD MOLECULES ENCODING
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001306DIV
CURRENT APPLICATION NUMBER: US/10/274,194
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                           US-10-274-194-4
; Sequence 4, Application US/10274194
; Patent No. 6706511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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545 LROVRDOONLP 555
                                                                                --ESFDOLDLP 567
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Best Local S
Matches 201
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Qy 299 EDVASHWWVN 314	: : Db 296 EQIMKDEWMNVGHEDDELKPYVEPLPDYKDPRRTELMVSMGYTREEIQDSLVGQRYNEVM 355	OY 315VGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFKOHVP 363	Db 356 ATYLLLGYKSSELEGDTITLKPRPSADLTNSSAPSPSHKVQRSVSANPKQR-R 407	Oy 364 GGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKS 419	ETGRKASSTAKVPASPLPG	Qy 420STSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSS 469	Db 464 TPTPSTNSVLSTSTNRSRNSPLLDRASLGQASIQNGKDST 503	Qy 470PEPSESGELLDASDVFVSGDPVEQKSPQASGLLLHRKGILKINGKFSRTALEG 522	Db 504 APQRVPVASPSAHNISSSSGAPDRTNFPRGVSSRSTFHAGQLRQVRDQQ 552	Qy 523 TTPSTFGSLDQLASSHPAARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVS 580	Db 553 NLPFGVTPASPSGHSQGRRG-PSGSIFSKFTSKFVRRULNEPESKDR 598	Qy 581 VDNLR 585	Db 599 VETLR 603	בי פיייטרני		; Sequence 35, Application US/09523849 ; Patent No. 6458561 ; ranconsamon	GENERAL INFORMATION; SPPLICANT: Bandman, Olda	; APPLICANT: Molteni, Angela ; APPLICANT: Magnachi, Paola	; APPLICANT: Bosotti, Roberta	; APPLICANT: Scacheri, Emanuela ; APPLICANT: Isacchi, Antonella	; APPLICANT: Hodgson, Dave ; TITLE OF INVENTION: HUMAN NIM1 KINASE	70 003/	T FILING DATE: 2	; NUMBER OF SEQ ID NOS: 39 ; SOFTWARE: PERL Program	35 604	; TYPE: PRT ; ORGANISM: Drosophila melanogaster		; OTHER INFORMATION: GenBank Accession No. 6458561 g2564680 ; FRATURE:	Er: unsure ON: 52, 291, 354	; OTHEK INFORMATION: UnKnown or other US-09-523-849-35	Query Match 19.8%; Score 653; DB 4; Length 604;	vative 76;	Qy 57 YEFLETLGKGTYGKVKKA-RESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNH 113			LENYLVKNGŘMRERDÁŘVLFŘO
Db 394LKVQRTISANQKQRRFSDHAGPSIPPAVSYTKRPQANSV 432	OY 458 KSRQRESGYYSSPEPSESGELLDASDVFVSGDPVEQKSPQ 497	Db 433 ESEQKEEWDKDTARRLGSTTVGSKSEVTASPLVGPDRKKSSAGPSNNVYSGGSMTRRNTY 492	Qy 498 ASGLILHRKGILKINGKFSRTALEGTTPSTFGSLDQLASSHPAARP 543	Db 493 VCERSTDRYAALQNGRDSSLTEMSASSMSSTGSTVASAGRSARP 536	RESULT 14	US-08-817-832B-32 ; Sequence 32, Application US/08817832B	Patent No. 6579691 GENERAL INFORMATION	APPLICANT: MANDELKOW, Eckhard, et al. TITLE OF INVENTION: No. 6579691el Protein Kinase (NPK-110)		** ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 S. Wacker Drive, 6300 Sears Tower	nicago Illinois	COUNTRY: US	3 2 2	COMPUTER: IBM PC compatible	SCHWARE Patentin Release #1.0, Version #1.30 (EPO)	CUKKENI APPLICATION UMBER: US/08/817,832B	PRIOR APPLICATION DATA:	APPLICATION NUMBER: WO PCT/EP95/04258 PILING DATE: 30-OCT-1995	PRIOR APPLICATION DATA:	999	FOR	LENGTH: 722 amino acids	ESS	; TOPOLOGY: linear ; MOLECULE TYPE: protein	2	5%; Score 673.5; DB 4; Length 722; 3%; Pred. No. 1.4e-49;	Matches 208; Conservative 88; Mismatches 212; Indels 157; Gaps	TADGLIKSPKPLMKKQAVKRHHHKHNLKHRYEFL	II ENEKUIDEVELLGGBUDS		120 HEVFENSKIVIVMEYASRCDI.7DYISRRPRISRRDARHFFROTUSAI.HYCHONGIUHRD	116 FEVIETEKTLYLWMEXASGGEVFDYLVAHGRKKEKERAAKFROTVSAVYCHHKETVHR	LKLENI LLDANGNI KI ADFGLSNLYHKGKFLQTFCGSPLYASPEI VNGKPYVGPEVDSWS	Db 176 LKAENLLLDADMNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPELFGGKKYDGPEVDVWS 235	Qy 240 LGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATL 298	

The state of the s

OY 504 HRKGILKINGKFSRTALEGTTPSTFGSLDQLASSHPAARP-SRPSGAVSEDSILSSESFD 562
563 QLDLPERLPETPLRGCVSVDNLRGLEQPPS-EGLKR 597 1

Search completed: January 22, 2005, 06:44:54 Job time : 43.6867 secs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

protein search, using sw model OM protein

Run on:

January 22, 2005, 06:29:16 ; Search time 38.5452 Seconds (without alignments) 1575.104 Million cell updates/sec

Title: Perfect score:

US-09-980-464-11 3293 1 MESVALLQRPSQAPSASALA......DCQEVTAAYRQALGICSKLS 631 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

IES	Description	otox latitod to the	ine/t	-5	probable serine/th	probable serine/th	protein H39E23.1 [hypothetical prote	serine/threonine-s	serine/threonine-s	gik protein - chic	probable serine/th	serine/threonine-s	serine/threonine-s	[hydroxymethylglut	FOG2 protein - yea	710	hypothetical prote	SNF-related kinase	probable serine/th	protein kinase - m	serine/threonine-s	probable serine/th	hypothetical prote	probable carbon ca	serine/threonine-s	protein kinase 1 -	protein kinase kin	serine/threonine p	serine/threonine-s
SUMMARIES	Ð	T29253	827966	G01025	148609	T18611	G89287	T13741	T52633	A26030	JC7500	T10449	JC1446	A56009	S51025	872513	A53621	T29858	B90100	T07415	149072	S59941	T07788	T20941	T41587	S44859	A38903	T40503	T04145	10
	DB		۱ ۸	7	~	7	7	7	7	П	7	7	H	Н	-	~	7	~	~	N	~	ч	N	~	~	-	~	~	N	П
	Length	15.50	7.7	745	774	1192	1246	1398	512	633	798	504	512	511	552	602	552	562	472	504	481	473	512	887	576	622	891	891	510	203
ð	Query Match	27.0		20.9		20.3		20.2	o,	φ.		19.5	6	19.2	6	ę.		18.9	8	ж	18.6	٠	в.	ъ.	ω.	7.	٠	17.7	۲.	17.3
	Score	888	694.5	689	686.5	699	667	664	649.5	648.5	648	641	639.5	631	630.5	2	623.5	622	621	620	612	610	599	96	9	87	583.5	8	579	570
	Result No.	-	101	٣	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18		20			23	24	25	26	27	28	29

SNF1-related prote	serine/threonine-s	serine/threonine-s	serine/threonine-s	probable protein k	serine/threonine-s	GIN4 protein - yea	p69Eg3 protein - A	probable serine/th	protein kinase KIN	probable serine/th	probable serine/th	probable protein k	hypothetical prote	SNF1-related prote	probable protein k
B90120	860303	560304	\$64930	C84667	S52687	859359	S52244	A86427	S29344	T14735	T14736	E84707	T33998	S62365	T02306
7	н	н	~	7	~	7	7	7	7	7	N	~	7	7	7
401	513	513	1147	441	1064	1142	651	480	800	440	440	435	726	746	502
17.3	17.1	17.1	17.0	16.7	16.7	16.6	16.6	16.5	16.5	16.4	16.3	16.2	16.1	16.0	15.9
569.5	564	563	559	549.5	549	547	545	543.5	543	539.5	537.5	534.5	529.5	527	524
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

hypothetical protein B0496.3 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 15-0cr-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999

C, Accession: T29253 R;Murray, J.; Le, T.T. Submitted to the EMBL Data Library, May 1996 A; Reference number: Z20596

A;Accession: T29253
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1558 <MUR>
A;Cross-references: EMBL:U58749; PIDN:AAB00636.1; GSPDB:GN00022; CESP:B0496.3
A;Experimental source: strain Bristol N2; clone B0496

C;Generics: A;Gene: CESP:B0496.3 A;Map position: 4 A;Introns: 55/1; 100/3; 141/1; 226/3; 298/1; 468/3; 502/2; 609/3; 656/3; 795/3; 843/2; 9

15; Query Match 27.0%; Score 888; DB 2; Length 1558; Best Local Similarity 37.0%; Pred. No. 2.1e-28; Matches 230; Conservative 73; Mismatches 214; Indels 104; Gaps

54 RHRYEFLETLGKGTYGKVKKARESS-GRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLN 112 :||:| : || ||||| | : | | ||:| | : ||: |||| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||: g ଚ

113 HPHIIAIHBVFENSSKIVIVMEXASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQ 172 õ g

173 NGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVG 232 ઠે 셤

g ò

312 ERRATIFDIASHWWLNLEENMPVIQELPENQIIDHTPLTEREETMIVQDLADEQDVFMEF 371 293 TRRATLEDVASHWWVNWGYTTGV-----------GEQEALREG 324 q à

--SSRPLLENGAKVCSFFKQHVPGGGSTV 369 372 GHLSSETRRKIEDPRIRRKEAREFNDNSPVKPPKARKTDELTGKISKEQPEEMKSAEKSL 431 GHPSGDFGRASMADWLRR-----325 ò 셤

370 PGLERQHS------LKKSRK-ENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKK 418 셤 ò

500 GLLLHRKGILKINGKESRTALEGTTPSTFGSLDOLASSHPAARP	Db 139 VHRDLKABENLILDADMNIKIADFGFSNEFTFGNKLDTFCGSPFYAAPELFQGKKYDGPEV 198 Qy 236 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPRFSDAC-GLIRMLLMVNPTR 294 Db 199 DVWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPRFSDAC-GLIRMLLMVNPTR 294 Qy 295 RATLEDVASHWWVNMGYTTGVGEGALREGGHPSGDFGRASMADWLRRSSRPLILENGAKY 354 Db 259 RGTLEQIMKDRWMNVGHEDDELKFYVBPLPDYKDPRRTELMVSMG 303 Qy 355 CSFFKQHVPGGSTVPGLERQHSLKKSRKENDMACNLQGDPAED 399 18:
Oy 419 SSTSSGEVOEDPOELRPVPDTGOPVPANSLLPRKGILKKERGRESGYYSSPERSEGEL 478 486 KEKSPEQOPEDPKTARGTSKRADSRAP-STVEVKURDETSEPERPRTRRH 534 OY 479 LDASDYPCSGEDVEKSPOASGLLLHRILM-GEFSTTAPTGGELDOLAS 536 Db 535 LTASARIETDSLAMLANQVLEQMEKGPVNLANIARIKAHPLYDTRPWKELLESIIA 592 OY 537 SHPAARPSRPSGAVSEDSILSSESPOQLDLPERLPETPERGCVSVDNLRGLEGEPS 592 SJ SHPAARPSRPSGAVSEDSILSSESPOQLDLPERLPETPERGCVSVDNLRGLEGEPS 592 OY 593 AGDEPVCKTYVROQTFSROWILTRKKKEDPLEEELPEVP	FLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEODLLHIRREIEIMSS

- Caeno

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A;Status: translated from GB/EMBL/DDBJ
A;Modecule type: DNA
A;Rodicuse 1-1192 - WHIL1>
A;Cross-references: UNIPROT:Q9TW45; EMBL:Z81027; PIDN:CAB54179.1; GSPDB:GN00023; CESP:H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 5
A;Introns: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 487/3; 535/3; 631/1; 825/2; 914/3; 992
C;Keywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific proc
F;1-1192/Product: probable serine/threonine-specific protein kinase, long splice form #8:
F;1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short splic
                                                                                                                                                                                                                      splice form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosidues: 1-1192 <#MIL.2
A;Cross-references: EMBL:206102; PIDN:CAB54263.1; GSPDB:GN00023; CESP:H39E23.1a
A;Experimental gource: clone H39E23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:296102; PIDN:CAB54262.1; GSPDB:GN00023; CESP:H39E23.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSPDB:GN00023; CESP:H39E23.1b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 AIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVH 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRA 296
                                                                                                                                                                                                                                                                                                                 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQAPSASALASESARPLADG-------LIKSPKPLMKKQAVKRHHHKHNLRHRYE
                                                                                                                                                                                      N.Contains: probable serine/threonine kinase (BC 2.7.1.-), long N.Contains: probable serine/threonine kinase, short splice form C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 09-Ju. R.McChurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.3%; Score 669; DB 2; Length 1192; 32.4%; Pred. No. 8.2e-20; ive 97; Mismatches 218; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN: CAB54178.1;
                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, October 1996
A,Reference number: 218997
A,Accession: T18611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R,McMurray, A.
submitted to the EMBL Data Library, June 1997
A,Reference number: Z19696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: translated from GB/EMBL/DDBJA; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: H39E23.1a; CESP: H39E23.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: clone H39E23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: clone AH10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Experimental source: clone AH10 Accession: T18610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-487,536-1192 <WIL2
A;Cross-references: EMBL:281027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 32.48 Matches 187; Conservative
                                                             561
                                                          RPSTAPORVP
   DQLDLPERLP
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   562
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                                                                                                                                                                                                                                                                                                                                                                                                      PIDN: CAA50040.1; PID: 957920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse chromosome
                                                                                                                                                                                                                19
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                                                C; Species: Mus musculus (house mouse)
C; Date: 02-Unl-1996 #text_change 16-Aug-2004
C; Accession: 148609; S31333
K; Inglis, J.D.; Lee, M.; Hill, R.E.
Mamm. Genome 4, 401-403, 1993
A; Title: Emk, a protein kinase with homologs in yeast maps to mouse chromosome A; Accession: 148609; MUD:93364122; PMID:8358177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 KQHVPGGGSTVPGL---ERQHSLKKSRKENDMAQNL-----QGDPAEDTSSRPGKSSLKL 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 PKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSP 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNSSAPSPSHKVQRSVSANPKQRR----SSDQAVFAI---PTSNSYSKKTQSNNAENKRP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NGKFSRTALEGTTPSTFGSLDQLASSHP-----AARPSRPSGAVSEDSILSSESF 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLQRPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHR----YEFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INERDTEOPTLGHLDS------KPSSKSNMLRGRNSATSADEQPHIGNYRLL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-699, Kr, 700-702, GRGLPTAAKASCTSGTCYCAGMAHQATRT', 731-774 <ING2>
A;Cross-references: BMBL:X70764
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : : | | | : : | | : : | EEETGRKASSTAKVPASPLDRKKTTPAPSTUSVLSTSTURSRUSPLLDRASLGQASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein
F;51-304/Domain: protein kinase homology <KIN>
F;59-67/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t
C
                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-774 < ING1>
A;Cross-references: UNITROT: 005512; EMBL:X70764; NID: 957919; PIDN: CA
R;Inglis, J.D.; Lee, M.; Hill, R.E.
submitted to the EMBL Data Library, January 1993
A;Description: A novel protein kinase with homologues in yeast maps
A;Reference number: S31333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103;
                             (EC 2.7.1.-) kem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.8%; Score 686.5; DB 2; Length 32.6%; Pred. No. 1.1e-20; tive 90; Mismatches 218; Indels
                          kinase
                             protein
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Matches 199; Conserv
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Qy : : : :	GVGBQEAL:	a & a & a & a	360KFEDIHATYLLLGERKSDMDASEITMAQSLLSHSSINVSSSLGQH- 404 408 LKLPKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLFRKGILKKKSRQRES 464 405PAGVITREHVTSSSASGSSASFRYSRSATATGASITAGSALASANAQKHQQSSA 461 465 GYYSSPEPSESGELLDASDVFVSGDPVEQKSPQASGLLLHRKGILKLNGKFSRTA 519 462 APSGSSSSRRSSQNDA-ATAAGGTVVMSGTRHGGVQMRAQPTSRQATISLLQPPSYKP 520 520 LEGTTPAGVISSLDQLASSHPAARPS 544	
Db 564 QKHQQSSAAPSGGSSS: Qy 512 NGKFSRTALEGTT Db 623 LQPPSYKPSSNTTQIA	: i i i i segssessessessonda-ataggetyvmsgtrhggvomraoptsroatisl 622 okhqossaapssgsssrrssgnda-ataggetsphaarps 544 ngkprtalegttpstpgsldolasshpaarps 544 loppsykpssmitqiaqipplenrnstatssaaqps 658	RESULT 7 T13741 hypotheti C;Species C;Date: 1 C;Accessi R;Murphy	<pre>cal protein 22E5.8 - fruit fly (Drosophila melanogaster) s: Drosophila melanogaster 3.Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004 L.; Harris, D.; Barrell, B.</pre>	
RESULT 6 G89287 protein H39E23.1 [imported] - Caenorhabditis elegan C,Species: Caenorhabditis elegans C,Species: 10-May-2001 C,Accession: G89287 R,anonymous, The C. elegans Sequencing Consortium.	ns #text_change 10-May-2001	Bubmitte A,Descrip A,Referer A,Access A,Status A,Molecu A,Residus	<pre>gubmitted to the EMBL Data Library, April 1999 A;Description: Sequencing the distal X chromosome of Drosophila melanogaster. A;Reference number: 217668 A;Reference number: 217668 A;Accession: T13741 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: Li198 <mur> A;Residues: 1-1398 <mur> A;Grose-references: UNIPROT:077268; EMBL:AL031765; NID:e1371523; PID:e1329905; PIDN:CAA2.)</mur></mur></pre>	. 2
Science 282, 2012-2018, 1999 A;Title: Genome sequence of th A;Reference number: A75500, A;Note: see websites genome.wu A;Note: published errata appea	: a platform for investigating biolog 11916 ;/ and www sanger.ac.uk/Projects/C_ele 15, 1999; Science 283, 2103, 1999; and	C;Genetic A;Cross-: A;Intron: A;Note::	ss: references: FlyBase:FBgn0000667 s: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3 gG:22E5.8	_
sion: G89287 3: preliminary 11e type: DNA 1es: 1-1246 <s 168:="" 168<="" 1es:="" td=""><td>TO> B:chr_V; PIDN:CAB09532.1; PID:g3878100; GSPDB:GN00023; CESP:H39E23.</td><td>Query Match Best Local S Matches 210 Qy 10</td><td>20.2%; Score 664; DB 2; Length 1398; imilarity 31.1%; Pred. No. 1.5e-19; Conservative 92; Mismatches 216; Indels 158; Gaps PSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYG </td><td></td></s>	TO> B:chr_V; PIDN:CAB09532.1; PID:g3878100; GSPDB:GN00023; CESP:H39E23.	Query Match Best Local S Matches 210 Qy 10	20.2%; Score 664; DB 2; Length 1398; imilarity 31.1%; Pred. No. 1.5e-19; Conservative 92; Mismatches 216; Indels 158; Gaps PSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYG	
A, Map position: 5 Query Match Best Local Similarity 31.9%;	%; Score 667; DB 2; Length 1246; %; Pred. No. 1e-19; 00. Minnetched 100. Tridels 96. Gang 16.	a & a	110 PGPSPTSSAVGAGGISGKDLLKLKEPMRVGFYD1EKTIGKGNFA 153 70 KVKKARES-SGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIHEVFENSSK 128	
	HILKHRYBELETLGKG 6	oy Dp		
	67 TYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIHEVFEN 125 	λ _o q	189 ANGNIKTADFGLSNLYHKGKFLOTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLYILV 248	
Oy 126 SSKIVIVMEYASRGDL :: : :: Db 129 EQTLYLVLEYASGGEV	SSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDLKLENI 185 : EQTLYLVLEYASGGEVFDYLVAHGRMKEKEARAKFRQIVSAVQYLHSKNIIHRDLKAENL 188	& 8	249 HGTMPFDGQDHKTLVKQISNGAYREPPKDSDAC-GLIRWLLMYNPTRRATLEDVASHWW- 306 1	
Qy 186 LLDANGNIKIADFGLS	LLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLY 245 : : :	oy G	307VNWGYTTGVGEQEALREGGHPSGDFGRASMADWL 340 393 CPELLEHVLIAKYNLGAERQTSVEPSEDILRI-MAEYVGIGSDKTRASLKKNTYDH 447	
Qy 246 ILVHGTMPFDGQDHKT : : Db 249 TLVSGSLPFDGQNLKE	ILVHGTMPFDGQDHKTLVKQISNGAYREPFKPSDAC-GLIRWLLMVNPTRRATLEDVASH 304	yo da	341RRSSRPLLENGAKVCSFFKQHVPGGG 366 448 VAAIYLLLQDRVSHKKEQSNGLGASALASSTSASRMIYSSRNDHQPTQQQSQQOSKTIST 507	1
Qy 305 WWVNWGYTTGVGEQEALREGGHPSGD- : : : Db 309 RWMNVGYEDDELKPFIEPPKDQ	305 WWVNWGYTTGVGEQEALREGGHPSGDFGRASWADWLRRSSRPL 347	Qy	367 STVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLP-KGILKK 417 	
Qy 348 LENGAKVCSFFKQHVE	348 LENGAKVCSFFKQHVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSS 407	λŏ	418 KSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSS 469 : :	-

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Sectine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana serine/threonine-specific protein kinase SNR1 homolog
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: JC1446; S58266; S66334
R; LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
R; LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
A; Reference number: JC1446; MUID:93013041; PMID:1339373
A; Accession: JC1446
A; Accession: JC1446
A; Accession: JC1446
A; Residues: 1-512 cLEG>
A; Thuemmler, F; Kirchner, M.; Teuber, R.; Dittrich, P.
B; Thuemmler, F; Kirchner, M.; Teuber, R.; Dittrich, P.
B; Thuemmler, F; Kirchner, M.; Teuber, R.; Dittrich, P.
Bubmitted to the EMBL Data Library, May 1995
A; Reference number: S58256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or peptidyl-threonine
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526 GQVMTGSPATARMTSAFLASQSDAPVLQVQGCMGGASLLPVSFQEGRRASDTSLTQGLKA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Molecule type: mRNA
A; Residues: 1-504 <GUN>
A; Cross-references: UNIPROT.P93113; EMBL:Y10036
A; Experimental source: cv. Masterpiece; cotyledon
C; Function:
A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidy
C; Superfamily: AMP-activated protein kinase; protein kinase homology
C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F; 6-260/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                      N.Alternate names: SNR1-related protein kinase (Species: Cucumis sativus (cucumber) 16-0ul-1999 #text_change 09-Jul-2004 (Spacession: T10449 (Spacession: T104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 YEFLETLGKGTYGKVKKARES-SGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRISERDARHFFRQIVSALHYCHQNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV
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                                                                                                                                                                                                                                                                                      probable serine/threonine-specific protein kinase (BC 2.7.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.4% Matches 127; Conservative
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RITIPEIRQHPW 259
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                                                                                                                               586 FRQQ 589
                                                                    598 WWQE 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 VKKARESSGRL-VAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIHEVFENSSKI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 VIVMEYASRGDLYDYISERPRISERDARHFFRQIVSALHYCHQNGIVHRDLKLENILLDA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLYILVH 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATLEDVASHWWWN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 WGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPL---LENGAKVCSFFKQHVPGG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNAEMPQDSLTSETLRSSLLYQQPQSLIQPSLQAEMDCDMNNPLQPVFFPVDPNFNGLFR 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LDLPERLPETPLRGCVSVDNL------RGLEQPPSEGLKR 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qin oncogene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEDASVPAPSAAQPRPLRVGF------39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dik protein - chicken

Gispecies: dallus gallus (chicken)

Rixia, Y: Zhang, Z:; Kruse, U:; Vogt, P.K.; Li, J.

Biochem: Biophys. Res. Commun. 276, 564-570, 2000

A;Title: The new serine-threonine kinase, Qik, is a target of the qin oncoge A;Accession: JC750

A;Contents: Embryo fibroblasts

A;Reference number: JC78

A;Accession: JC78

A;Residues: 1-78

A;Residues: 1-78

A;Residues: 1-78

A;Residues: 1-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9IA88; GB:AF219232
C;Comment: This protein, a member of the AMPK/SNF1 family of
C;Genetics:
A;Gene: qik
C;Keywords: protein kinase
                                             499
                                                                                                            KSHQKS 427
                                                 KSPOAS
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7

Length 511;

19.2%; Score 631; DB 1; 49.6%; Pred. No. 1.2e-18; tive 48; Mismatches 77;

78

235

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-511 <MUR>
A;Cross-references: UNIPROT:Q40544; GB:D26602; NID:g496384; PIDN:BAA05649.1; PID:g496385
C;Function:
                                                                                                                                             A)Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C;Superfamily: AMP-activated protein kinase; protein kinase homology C;Keywords: ATP; magnesium; phosphotransferaes; serine/threonine-specific protein kinase P;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 YEFLETLGKGTYGKVKKARES-SGRLVAIKSIRKDKIKDEQDLLHIRREJEJMSSLNHPH 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPS-DACGLIRWLLMVNPTR 294
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A;Reference number: A56009; MUID:94217693; PMID:8164654
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 49.69
Matches 125; Conservative
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RMTIPEIRMHPW 270
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A, Residues: 144-198 - TH2>
A, Cross-references: EMBL:X86966; NID:9928909; PIDN:CAA60529.1; PID:9928910
C, Comment: This enzyme plays an important role in a signal transduction cascade regulatic Genetics:
A, Gene: AKinlo; AK21
A, Gene: AKinlo; AK21
A, Filtrans: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C, Function:
A, Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C, Superfamily: AMP-activated protein kinase; protein kinase homology C, Reywords: ATP; magnesium; phosphotransferaes; serine/threonine-specific protein kinase F;17-271/Domain: protein kinase homology KIN>
F;17-371/Domain: protein kinase homology KIN>
F;15-331/Region: protein kinase ATP-binding motif F;48, 67, 142, 144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
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                                                                                                                                                   22 novel protein kinase
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35.8%; Pred. No. 5.5e-19;
tive 72; Mismatches 139;
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156; Conservative
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                                                                                                                                                                                                                                                                                                                                    A; Title: Molecular cloning, expression and chromosomal localisation of human AMP-activat A; Reference number: S51025; MUID:95080410; PMID:7988703
                                   N'Alternate names: AMPK
N'Alternate names: AMPK
N'Contains: [acetyl-CoA carboxylase] kinase (EC 2.7.1.128); [hydroxymethylglutaryl-CoA C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51025; IBS503
R;Berli, R.K.; Marley, A.E.; See, C.G.; Sopwith, W.F.; Aguan, K.; Carling, D.; Scott, J. PEBS Lett. 356, 117-121, 1994
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hydroxymethylglutaryl-CoA reductase (NADPH2)} kinase (EC 2.7.1.109) - human
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A;Residues: 1-179,'T',181-270,'G',272-402,'RQ',405-552 <RES>
A;Cross_references: EMBL:U06454; NID:9758366; PIDN:AAA64745.1; PID:9758367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the
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A,Residues: 1-552 <BBR>
A,Cross-references: UNIPROT:P54646
R;Aguan, K.; Scott, 19; See, C.G.; Sarkar, N.H.
Gene 149, 345-350, 1994
A,Title: Characterization and chromosomal localization o
A,Reference number: I38503; MUID:95047501; PMID:7959015
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A;Cross-references: GDB:451905; OMIM:600497
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Serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco. Progress: Nicotiana tabacum (common tobacco)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C;Accession: A56009
R;Muranaka, T: Banno, H: Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces

tase of Saccharomyces cerevisiae

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F;33-286/Domain: protein kinase homology <KIN>
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               C; Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase F:14-268/Domain: protein kinase homology «KIN»
F:22-30/Region: protein kinase ATP-binding motif F:22-30/Region: protein kinase ATP-binding motif F:45.64,139,141/Active site: Lys, Glu, Asp, Lys #status predicted F:144,148/Binding site: magnesium (Asn, Asp) #status predicted
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C,Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C,Bate: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C,Bate: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C,Accession: 872511, A.; Donnini, C.; Lodi, T.; Puglisi, P.P.; Ferrero, I.
R,Goffrini, P.; Ficarelli, A.; Donnini, C.; Lodi, T.; Puglisi, P.P.; Ferrero, I.
A,Title: FOGI and FOGS genes, required for the transcriptional activation of glucose-rep A,Reference number: 872513; MUID:96171514; PMID:8598052
A,Accession: 872513
A,Accession: S72513
A,Accession: Lody compared with conceptual translation
A,Accession: Lody compared with conceptual translation
A,References: UNIPROT:P87209
A,Cross-references: UNIPROT:P87209
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C.Genetics:
A.Gene: FOG2
C.Function:
A.Description: probably involved in the regulation of glucose-repressible gene expressic
C.Superfamily: AMP-activated protein kinase; protein kinase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 ESEVMNSLYSGDPQ---DQLAVAYHLIIDNRRIMNQASE---FYLASSPPSGSFMDDSAM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 HIPPGLKPHPERMPPLIADSPKARCPLDAL------NTTKPKSLAVKKAKWHLGIR 407
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Superfamily: AMP-activated protein kinase; protein kinase homology
                                                                                                                                                                                              93;
                                                                                                                                                    DB 1; Length 552;
                                                                                                                                               Query Match
19.1%; Score 630.5; DB 1; Length 5
Best Local Similarity 31.5%; Pred. No. 1.3e-18;
Matches 176; Conservative 91; Mismatches 199; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 PDYLVPAESTHQENS-----ESKTEDGGPSVPLELIDDSLVQTLSNTMGYDVDEIYEA 343
                                                                                                                                                                                                                99 L-HIRREIEIMSSLNHPHIIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDAR 157
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                                                                                                                                          HFFRQIVSALHYCHQNGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSP
                                                                                                         47 HHHKHNLRH-----RYEFLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDL
                                                       Gaps
                                                    87;
     Length 602;
                                                       Indels
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SQGAASLIKKMLIVNPVNRITVHEIMQDEWF------
19.1%; Score 627.5; DB 2;
llarity 35.6%; Pred. No. 1.9e-18;
Conservative 68; Mismatches 125;
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he : 42.5452 secs
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                      Best Local Similarity
Matches 155; Conserv
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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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sequence 103, App Sequence 20, Appl Sequence 20, Appl Sequence 102, App Sequence 102, Appl Sequence 102, Appl Sequence 29, Appl Sequence 2, Appli Sequence 7, Appl Sequence 7, Appl Sequence 72, Appl Sequence 73, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 27, Appl
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Best Local Similarity 100.0%; Pred. No. 1.4e-206;
Matches 631; Conservative 0; Mismatches 0; Indels 0;
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Publication No. US20030162277A1
GENERAL INFORMATION:
APPLICANT: Used, Timothy A.
APPLICANT: Wirca, G. Duke
APPLICANT: Wirca, G. Duke
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-A
CURRENT APPLICATION NUMBER: US/10/355,975
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US/09/579,664B
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
SOUTHWARE: Patentin version 3.1
SEQ ID NO!
4 US-10-354-358-82

10S-10-723-866-2553

10S-10-836-392-40

10S-10-343-514-103

10S-10-343-514-102

10S-10-343-514-102

10S-10-343-514-102

10S-10-343-514-102

10S-10-343-514-102

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10S-10-258-106-16

10S-10-258-106-16

10S-10-258-106-16

10S-10-258-106-16

10S-10-258-106-16

10S-10-26-45-8

10S-10-161-565-28

10S-10-195-101-33

10S-10-143-54-47
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US-10-425-114-70100
US-09-919-585-3
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; ORGANISM: Mus musculus
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1301.5
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Sequence 44, Appl
Sequence 44, Appl
Sequence 640, Appl
Sequence 77, Appl
Sequence 12, Appl
Sequence 26, Appl
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Sequence 404, App
Sequence 504, App
Sequence 2, Appli
Sequence 6, Appli
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Sequence 23,
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1: \cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: \cgn2_6/ptodata/1/pubpaa/PCT_MBW_PUB.pep:*
3: \cgn2_6/ptodata/1/pubpaa/NG0_NBW_PUB.pep:*
4: \cgn2_6/ptodata/1/pubpaa/US06_NBW_PUB.pep:*
5: \cgn2_6/ptodata/1/pubpaa/US06_NBW_PUB.pep:*
6: \cgn2_6/ptodata/1/pubpaa/US08_NBW_PUB.pep:*
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9: \cgn2_6/ptodata/1/pubpaa/US08_NBW_PUB.pep:*
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19: \cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                   GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-370-715B-640
US-10-61B-941-77
US-10-311-034-12
US-10-322-281-26
US-10-353-829-504
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US-10-322-281-23
US-10-343-514-41
US-09-963-159-2
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US-09-780-949-6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match
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Result No.

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APPLICANT: BRUCKER, Daniel J.
APPLICANT: ROSEN, Cheryl F.
APPLICANT: ROSEN, Cheryl F.
TITLE OF INTENTION: AMPR.RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
TITLE OF INTENTION: AMPR.RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REFERRING: DAA-DRUCZ/PCT
CURRENT APPLICATION NUMBER: US/10/343,514
CURRENT FILING DATE: 2003-01-31
PRIOR PELING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PELING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/274,613
PRIOR PELING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: CA 2,340,780
PRIOR PILING DATE: 2001-03-28
NUMBER OF SEC ID NOS: 109
SOFTWARE: PATENTING DATE: 2001-03-28
NUMBER OF SEC ID NOS: 109
SEC ID NO 41
LENGTH: 630
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GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED
                                                                                                                                                            310 VASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFKQ
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                                                        GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED
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Best Local Similarity
Matches 593; Conserva
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                                                                                                                                                                          GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED
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                  KLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL
                                                                                          KLENI LLDANGNI KIADFGLSNLYHKGKFLQTFCGSPLYASPEI VNGKPYVGPEVDSWSL
                                                                                                                                                  GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED
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US-10-322-281-23

// Sequence 23, Application US/1032281

// Sequence 23, Application US/1032281

// Publication No. US20040126762A1

// GENERAL INFORMATION:

// APPLICANT: David W. Morris

// APPLICANT: Marc S. Malandro

// TILE OF INVENTION: Novel Compositions and Methods in Cancer

// FILE REFERENCE: 529452001000

// CURRENT APPLICATION UNDRER: US/10/322,281

// CURRENT FILING DATE: 2002-12-17

// NUMBER OF SEQ ID NOS: 866

// SEQ ID NO 23
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98.3%; Pred. No. 1.4e-199;
tive 0; Mismatches 1;
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Matches 620; Conservative
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ORGANISM: Mus musculus
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US-10-322-281-23
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Sequence 4, Application US/10423543

Publication No. US20040058355A1

SEQUENCE AL INPORMATION:

APPLICANT: Milbermann, Rosena K.

APPLICANT: Milbermann, Rosena K.

APPLICANT: Hunter, John J.

APPLICANT: Radiph-Owen, Laura A.

APPLICANT: Radiph-Owen, Laura A.

APPLICANT: Curtis, Rory A.J.

APPLICANT: Teal, Foog-Ying

APPLICANT: Teal, Foog-Ying

APPLICANT: Glain, Majoung

APPLICANT: Glain, Majoung

APPLICANT: Bandaru, Rajaesha, 56634, 55053, 2504, 15977,

APPLICANT: Bilos-Santisgo, Inmaculada

APPLICANT: Milliamson Mark J.

APPLICANT: Bilos-Santisgo, Inmaculada

BRIOR PILING DATE: 2000-11-13

PRIOR APPLICANT: WIMBER: US 60/248, 933

PRIOR APPLICANT: WIMBER: US 60/248, 933

PRIOR APPLICATION NUMBER: US 60/248, 933

PRIOR APPLICATION NUMBER: US 60/248, 933

PRIOR APPLICATION NUMBER: US 60/248, 933
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                                                                                                             541 ARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSVDNLRGLEQPPSEG----LK
        KLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL
                                KLENI LLDANGNI KIADFGLSNLYHQGKFLQTFCGSPLYASPEI VNGKPYTGPEVDSWSL
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                                                                                       HVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKSS 420
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Factor No. US2002007312A1
GENERAL INFORMATION:
FAPPLICANT: Cutris, Rory A.J.
APPLICANT: Galvin, Katherine M.
TILLE OF INVENTION: 3700, A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR FILE REFRENCE: 10147-5001.
CURRENT APPLICATION NUMBER: US/09/963,159
CURRENT FILING DATE: 2001-09-25
FRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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85.8%; Score 2824.5; DB 9;
Best Local Similarity 85.7%; Pred. No. 5.4e-176;
Matches 544; Conservative 26; Mismatches 54; I
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; ORGANISM: Homo sapiens
US-09-963-159-2
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                                                                           or
                                                                                                                                                                                                  Query Match

85.8%; Score 2824.5; DB 15; Length
Best Local Similarity 85.7%; Pred. No. 5.4e-176;
Matches 544; Conservative 26; Mismatches 54; Indels
                                                                        File
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PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/186,061
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 10/217,168
PRIOR FILING DATE: 2002-08-12
Remaining Prior Application data removed - S.
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 44
                                                                                                                                                          ORGANISM: Homo Sapiens
                                                                                                                                                                       US-10-423-543-44
                                                                                                                             LENGTH: 628
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Sequence 640, Application US/10370715B
Publication No. US20040258678A1
GENERAL INFORMATION:
Patin Docket Preview
APPLICANT: CDARK,HILLARY
APPLICANT: CLARK,HILLARY
APPLICANT: JACKMAN,JANET

RESULT 6 US-10-370-715B-640

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||||| MESLVFARRSGPTPS----AAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL
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              APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD WILLIAM I.
APPLICANT: WOOD WILLIAM I.
APPLICANT: WOOD WILLIAM I.
TITLE OF INVENTION: Compositions and Methods for the Treatment of I TITLE OF INVENTION: Related Diseases
FILE REFERENCE: P1948R1-US
CURRENT APPLICATION NUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 640
                                                                                                                                                                                                                                                                        85.8%; Score 2824.5; DB 17; Length 628;
85.7%; Pred. No. 5.4e-176;
iive 26; Mismatches 54; Indels 11;
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SCHOENFELD, JILL R. WILLIAMS, P. MICKEY WOOD, WILLIAM I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: CAENEPEEL, SEAN
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.7<sup>3</sup>
Matches 544; Conservative
                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                           US-10-370-715B-640
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APPLICANT: LO, Terence P.
APPLICANT: KRHH, Farrah A.
APPLICANT: KRHH, Farrah A.
APPLICANT: KRHH, Farrah A.
APPLICANT: KRHH, Farrah A.
APPLICANT: KECIPON, Shirley A.
APPLICANT: POLICKY, Jennifer L.
APPLICANT: POLICKY, Jennifer L.
APPLICANT: PLIOT, Vicki S.
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: TRANGAVELU, Kavitha
APPLICANT: ISON, Craig H.
APPLICANT: BATRA, Sajeev
APPLICANT: BATRA, Sajeev
APPLICANT: TRANGAVELU, Kavitha
APPLICANT: TOURENT APPLICATION NUMBER: US/10/311,034
CURRENT APPLICATION NUMBER: 60/212,073; 60/213,467; 60/216,665; 60/218,372; 60/228,066
PRIOR APPLICATION OF STATEMENT ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DACGLIRWLLMVNPTRRATLEDVASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASMAD 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DACGLIRWLLMVNPTRRATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 LHIRREIEIMSSLNHPHIIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 YASPEIVNGKPYTGPEVDSWSLGVLLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 MKKQAVKRHHHKHNLRHRYEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:

NAME/KEY: misc feature

CTHER INFORMATION: Incyte ID No. US20040023242A1 4841542CD1
US-10-311-0334-12
                                                     GANDHI, Ameena R.
TRIBOULEY, Catherine
CHAWLA, Narinder K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAFALIA, April
ARVIZU, Chandra S.
GURURAJAN, Rajagopal
                                                                                                                                                                                                                  RAMKUMAR, Jayalaxmi
GRIFFIN, Jennifer A
KEARNEY, Liam
                                                                                                                                   YAO, Monique G.
LU, Dyung Aina M.
GREENWALD, Sara R.
                                                                                                                                                                                                                                                                                                                          NGUYEN, Danniel B.
TANG, Y. Tom
BAUGHN, Mariah R.
                                                                                                                                                                                                                                                                                                                                                                                                           HE, Ann
THORNTON, Michael
                                                                                                                                                                                                                                                                                                         Neil
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SOFTWARE: PERL Program
SEQ ID NO 12
LENGTH: 594
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ORGANISM: Homo sapiens
                   GANDHT
                                                                                                                                                                                                                                                                                                   BURFORD,
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 EVFENSSKIVIVMEYASRGDLYDYISERQQLSEREARHFFRQIVSAVHYCHQNRVVHRDL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 GVLLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFKQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 HAPGGGSTTPGLERQHSLKKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPKGILKKKVS 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                            1 85.8%; Score 2824.5; DB 17; Length 672; Similarity 85.7%; Pred. No. 5.9e-176; 14; Conservative 26; Mismatches 54; Indels 11;
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CURRENT APPLICATION NUMBER: US/10/618,941
FULL REPAIR APPLICATION NUMBER: 00/395,632
PRIOR APPLICATION NUMBER: 60/395,632
NUMBER OF SEQ ID NOS: 143
SEQ ID NO 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 12, Application US/10311034
; Publication No. US20040023242A1
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
TITLE OF INVENTION: NOVEL KINASES
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.73
Matches 544; Conservative
                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                   ; ORGANISM: HOI
US-10-618-941-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-311-034-12
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FEATURE:

NAME/KEX: misc_feature

OTHER INFORMATION: Incyte ID No: LG:982800.1.orf1:2000SEP08
US-10-363-829-404
                                                                                                                                                                                                                    RWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS
                                                                                                                                                                                                                                                                                                                    Sequence 404, Application US/10363829
Publication No. US20040142331A1
GENERAL INFORMATION:
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ORGANISM: Homo
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121
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                                 459 SRQRESGYYSSPEPSESGELLDASDVFVSGDPVEQKSPQASGLLLHRKGILKLNGKFSRT 518
                                                                                                                                                                     418 PRQRESGYYSSPEPSESGELLDAGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQT 477
                                                                                                                                                                                                                  519 ALEGTIPSTFGSLDQLASSHPAARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGC 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETLGKGTYGKVKKARRESGGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHIIAIH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 VASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFKQ 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MESLVFARRSGPTPS----AAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL 56
                                                                                                                                                                                                                                                                                                   579 VSVDNIRGLEQPPSEG----LKRWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
                                                                              TSSRPGKSSLKLPKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKK
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/1032281
| Sequence 26, Application US/1032281
| Publication No. US20040126762A1
| GENERAL INFORMATION:
| APPLICANT: David W. Morris
| APPLICANT: David W. Morris
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer
| CURRENT APPLICATION WUMBER: US/10/322,281
| CURRENT FILING DATE: 2002-12-17
| WUMBER OF SEQ ID NOS: 866
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 26
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82.4%; Score 2712.5; DB 16; Length
Best Local Similarity 84.3%; Pred. No. 1.1e-168;
Matches 535; Conservative 25; Mismatches 52; Indels
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US-10-322-281-26
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                                                   TSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPSESGELLD
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APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
APPLICANT: Chalup, Michael S.; V. Jackson, Jennifer L.;
APPLICANT: Chalup, Michael S.; V. Jackson, Jennifer L.;
APPLICANT: Wright, Rachel J.; Girtzen, Darryl;
APPLICANT: Bradley, Diana L.; Roheser, Darryl;
APPLICANT: Bradley, Diana L.; Roheser, Lincoln, Ann M.;
APPLICANT: Geretin, Jr.; Edward H.; Peralta, Careyna H.;
APPLICANT: Geretin, Jr.; Edward H.; Peralta, Careyna H.;
APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
APPLICANT: Inman, Rabekah R.
APPLICANT: Inman, Rabekah R.
ITILE OF INVENTION: WOLECULES FOR DISEASE DETECTION AND TREATMENT FILM DATE: 2003-035
PRIOR PRING APPLICATION NUMBER: US (0/229,75)
PRIOR APPLICATION NUMBER: US (0/229,75)
PRIOR APPLICATION NUMBER: US (0/229,74)
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-06
PRIOR PRIOR PRIOR PRIOR PRIOR PRIO
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SOFTWARE: PERL Program
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Patent No. US20020006618A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Liberman, Rosana
APPLICANT: Galvin, Katherine M.
TITLE OF INVENTION: Methods for Using 20893, a Human Protein
TITLE OF INVENTION: Methods for Using 20893, a Human Protein
TITLE OF INVENTION: Kinase
FILE REFERENCE: 035800/209015
CURRENT FILING DATE: 2001-02-09
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,690
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 6
SO ID NO 2
LENGTH 661
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NAME/KEX: misc_feature

CTHER INFORMATION: Incyte ID No: LI:1144409.1.orf1:2000SEP08
US-10-363-829-504
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PRIOR APPLICATION NUMBER: US 60/230,010
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: US 60/230,597
PRIOR FILING DATE: 2000-09-06
Remaining Prior Application data removed - %
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PERL Program
SOFTWARE: AAA
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: H. E
US-09-780-949-2
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US-09-780-949-2
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                                                                           Gaps
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APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Jones, Aniesa L.; Yu, Jimmy Y.;
APPLICANT: Liu, Trommy F.; Yap, Pierre E.;
APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Bradley, Diana L.; Robatgi, Sameer D.;
APPLICANT: Bradley, Diana L.; Robatgi, Sameer D.;
APPLICANT: Geretin, Jr.; Edward H.; Peralta, Careyna H.;
APPLICANT: Geretin, Jr.; Edward H.; Peralta, Careyna H.;
APPLICANT: Geretin, Jr.; Edward H.; Peralta, Careyna H.;
APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
APPLICANT: Towny V.; Robel,
APPLICANT: Towny V.; Robel,
APPLICANT: Towny V.; Boward R.
APPLICANT: Towny V. V.
APPLICANT: Towny V.
APPLICA
      54.1%; Score 1781.5; DB 16; Length 406; 83.6%; Pred. No. 4.1e-108; ive 16; Mismatches 44; Indels 7;
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                                     Best Local Similarity 83.6
Matches 342; Conservative
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US-09-780-949-6

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ARES-SGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIHEVFENSSKIVIV 132
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                                                                                                                                                                             LP-ETPLRGCVSVDN-----LRGLEQPPSEGLKRWWQESLGDSCFS-LTDCQEVTAAYR 621
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                                                                        13 PDLGLGAPGSPREAVAGATAALEP-RKPHGVKRHHHKHNLKHRYELQETLGKGTYGKVKR
                                                                                                                                                                                                                      IKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLYILVHGTM
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                  Gaps
                73;
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                Indels
al Similarity 55.5%; Pred. No. 1.7e-102; 372; Conservative 74; Mismatches 151;
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Patent No. US2002006618A1
GENERAL INFORMATION:
APPLICANT: Rapeller-Liberman, Rosana.
APPLICANT: Meich, Nadine S.
APPLICANT: Meich, Nadine S.
APPLICANT: Galvin, Katherine M.
TITLE OF INVENTION: Kinase
FILE REFERENCE: 015800/209015
CURRENT APPLICATION NUMBER: US/09/780,949
CURRENT APPLICATION NUMBER: US 60/181,690
PRIOR APPLICATION NUMBER: US 60/181,690
PRIOR PRIOR SEQ ID NOS: 6
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 661
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ORGANISM: H. sapiens
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US-09-780-949-6
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| Sequence 82, Application US/10354358 | Publication No. US20030157082A1 | Sequence 82, Application No. US20030157082A1 | GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: Millamium Pharmaceuticals, Inc |
| APPLICANT: Hunter, John Joseph |
| APPLICANT: Honter, John Joseph |
| APPLICANT: Hondrea |
| APPLICANT: Lescon, Andrea |
| APPLICANT: Lightcap, Eric S |
| APPLICANT: Lightcap, Eric S |
| APPLICANT: Millamson, Mark |
| APPLICANT: Rudolph-Owen, Laura A |
| TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2689, 2427, 3702, 5891, 6428, |
| TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235, |
| TITLE OF INVENTION: 3703, 1411, 10359, 1660, 1450, 18894, 2088, 32427, 2160, |
| TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469, |
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                                 18;
                                                                                                                        PFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLEDVASHWWVNWGYT 312
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                                                              14 PSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYGKVKK
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                               73;
 Length 661
                                 Indels
 DB 9;
                               74; Mismatches 151;
51.6%; Score 1699.5; DB 9 55.5%; Pred. No. 1.7e-102;
              Similarity 55.53
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APPLICANT: Aziz, Natasha
APPLICANT: Ginburg, Wendy M.
APPLICANT: Ginburg, Wendy M.
APPLICANT: Ginburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: MOUBER: US/10/723,860
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 2553
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                                                EGTTPS----TFGSLDQ-----LASSHPAARPSRPSGAVSEDSILSSESFDQLDLPER
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Pred. No. 1.7e-102;
                                                                                                                                                                                                                                                                                                                                                                                Sequence 2553, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
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55.5%;
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Best Local Similarity 55.5%
Matches 372; Conservative
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                                                                                                                                                                                                                                                           QALEICSKLN 661
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US-10-723-860-2553
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TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943, TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099, TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES: FILE REFERENCE: MPIO2-020PIRNOMIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFKQHVPGGGSTVPGL 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73;
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                                                                              TLUE KEFERENCE: MAIOL 2020 PROVINCE TO COURRENT APPLICATION NUMBER: US/10/354,358 CURRENT FILING DATE: 2003-01-30 PRIOR PELLING DATE: 2003-01-30 PRIOR PELLING DATE: 2003-01-31 PRIOR FILING DATE: 2002-03-15 PRIOR PELLON NUMBER: US 60/371,075 PRIOR PELLON NUMBER: US 60/371,075 PRIOR APPLICATION NUMBER: US 60/371,507 PRIOR APPLICATION NUMBER: US 60/371,507 PRIOR APPLICATION NUMBER: US 60/372,984 PRIOR FILING DATE: 2002-04-10 PRIOR FILING DATE: 2002-04-10 PRIOR PELLON DATE: 2002-04-19 PRIOR PELLON DATE: 2002-04-19 PRIOR PELLON NUMBER: US 60/382,995 PRIOR FILING DATE: 2002-04-19 PRIOR FILING DATE: 2002-05-24 PRIOR FILING DATE: 2002-05-24 PRIOR FILING DATE: 2002-05-31 PRIOR FILING DATE: 2002-05-31 PRIOR APPLICATION NUMBER: US 60/388,853 PRIOR APPLICATION NUMBER: US 60/388,853 PRIOR FILING DATE: 2002-06-17 PRIOR FILING DATE: 2002-06-17 PRIOR FILING DATE: 2002-06-17 PRIOR FILING DATE: 2002-06-17
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        Qy
        467 YSSPEPSESGELLDASDVFVSGDPVEQKSP-----QASGLLLHRKGILKLNGKFSRTAL 520

        Db
        479 YSSPERSESSELLDSNDVM-GSSIPPSPRPARVTSHSLSCRRKGILKHSSKYSAGTM 536

        Qy
        521 EGTTPS----TFGSLDQ-----LASSHPAARPSRPSGAVSEDSILSSESFDQLDLPER 569

        Db
        537 DPALVSPEMPTLESLSEPGVPAEGLSRSY----SRPSSVISDDSVLSSDSFDLLDLQEN 591

        Qy
        570 LP-ETPLRGCVSVDN-----LRGLEQPPSEGLKRWWQESLGDSCFS-LTDCQEVTAAYR 621

        Db
        592 RPARQRIRSCVSAENFLQIQDFEGLQNRPRQYLKRYRNRLADSSFSLLTDMDDVTQVYK 651

        Qy
        622 QALGICSKLS 631

        CS2 QALGICSKLS 631

        Db
        652 QALEICSKLN 661
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Search completed: January 22, 2005, 07:00:33 Job time : 150.329 secs